



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 143545

TO: Vanessa L Ford
Location: REM/3B25/3C18
Art Unit: 1645
Friday, January 28, 2005.

Case Serial Number: 10/017168

From: Edward Hart
Location: Biotech-Chem Library
REM-1A55
Phone: 571-272-2512

edward.hart@uspto.gov

Search Notes

Examiner Ford,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart

From: Chan, Christina
Sent: Thursday, January 27, 2005 3:16 PM
To: Ford, Vanessa; STIC-Biotech/ChemLib
Subject: RE: In re: 10/017168 sequence search

Please rush. Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89

-----Original Message-----

From: Ford, Vanessa
Sent: Thursday, January 27, 2005 1:40 PM
To: Chan, Christina
Subject: In re: 10/017168 sequence search

Please search the SEQ ID NOS: 2, 9, 11, 12, 13, 14, 15, 16, 17 and 18. Please include interferences. Please rush.

Vanessa L. Ford
Biotechnology Patent Examiner
Office: REM 3B25
Mailbox: REM 3C18
Phone: 571.272.0857
Art Unit:1645

1/27/2005
(STIC)
1/27/2005

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2-
Date Searcher Picked up: *1/28/05*
Date Completed: *1/28/05*
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search
NA Sequence: # _____
AA Sequence :# *10*
Structure: _____
Bibliographic: _____
Litigation: _____
Patent Family: _____
Other: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: *QDP*
WWW/Internet: _____
Other(Specify): _____

Copyright (c) 1993 - 2005 Compugen Ltd.	GenCore - version 5.1.6			
OM protein - protein search, using sw model				
Run on: January 28, 2005, 11:12:20 ; Search time 379.116 Seconds	(without alignments)			
US-10-017-168-2	655.635 Million cell updates/sec			
Perfect score: 2188				
Sequence: 1 MFRSDMPKNTAVENSL MTKQPSHSVSNSAPNQFRKP 432				
Scoring table: BLOSUM62				
Gapop 10.0 , Gapext 0.5				
Searched: 1825181 seqs, 575374646 residues				
Total number of hits satisfying chosen parameters: 1825181				
Minimum DB seq length: 0				
Maximum DB seq length: 2000000000				
Post-processing: Minimum Match 0% ; Maximum Match 100%				
Listing first 45 summaries				
Database : UniProt 02;*				
1: uniprot_sprot;*				
2: uniprot_trembl;*				
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.				
SUMMARIES				
Result No.	Score	Query Match length	DB ID	Description
1	2188	100.0	432	051953
2	2178	99.5	548	093CA4
3	1475	67.4	428	09ALV6
4	1286.5	58.8	393	093CA3
5	1043.5	47.7	348	09ALV7
6	96.7	44.2	256	083449
7	47.9	21.9	227	083449
8	368.5	16.8	458	073NG7
9	368.5	16.8	458	2 AAS1704
10	285.5	13.0	1108	2 AAS1704
11	279	12.8	5458	2 09U459
12	268	12.2	2768	2 09VC00
13	267.5	12.2	432	2 0964C9
14	267.5	12.2	721	1 YCF2_OBNPI
15	264.5	12.1	843	2 06GLW0
16	264.5	12.1	897	2 013098
17	260	11.9	913	2 013099
18	260	11.9	913	2 06DC00
19	260	11.9	1110	2 091255
20	255	11.7	466	2 06NE60
21	255	11.7	572	2 CABE12033
22	255.5	11.7	474	2 0942KB
23	255.5	11.7	567	2 09HD28
24	254.5	11.6	248	2 09LRH2
25	252.5	11.6	167	2 07SH94
26	251.5	11.5	1394	1 CNG4_BOVIN
27	249.5	11.4	572	2 08MKF9
28	248.5	11.4	3455	2 06R5A9
29	248.5	11.4	3455	2 AAR97872
30	248	11.3	1070	2 081Y0
31	11.3		1070	2 Aat2649_bacillus
32				Q26893 trypanosoma
33				Q73cu8 bacillus ce
34				AA39897 bacillus
35				Q8pc82 brachydano
36				AAB59189 brachydano
37				Q26899 trypanosoma
38				Q25860 plasmodium
39				Q801t3 xenopus lae
40				Q80bk7 saimirine
41				Q7rmx1 plasmodium
42				Q81hn3 plasmodium
43				Q80ag4 saimirine
44				Q96g11 fugu rubrip
45				Q962i4 encephalito
				ALIGNMENTS
RESULT 1				
ID 051953				PRELIMINARY;
AC 051953;				PRT;
DT 01-JUN-1998 (TREMBREL 06, Created)				432 AA.
DT 01-JUN-1998 (TREMBREL 06, Last sequence update)				
DT 01-OCT-2002 (TREMBREL 22, Last annotation update)				
DE Acidic repeat protein.				
OS Treponema pallidum.				
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.				
OX NCBI_TaxID=160;				
RN [1]				
RP				
RC				
RA Steiner B.M., Liu H., Rodes B.;				
RA Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.				
DR EMBL: AP015824; AAB94541.1; -;				
SEQUENCE 432 AA; 46364 MM; 8F81E4C55CB46A23 CRC64;				
Query Match 100.0%; Score 2188; DB 2; Length 432;				
Best Local Similarity 100.0%; Pred. No. 4.2e-104; Mismatches 0; Indels 0; Gaps 0;				
Matches 432; Conservative 0; N.A.				
SEQUENCE FROM N.A.				
STRAIN=richards; Liu H., Rodes B.;				
RA Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.				
DR EMBL: AP015824; AAB94541.1; -;				
SEQUENCE 432 AA; 46364 MM; 8F81E4C55CB46A23 CRC64;				
Query Match 100.0%; Score 2188; DB 2; Length 432;				
Best Local Similarity 100.0%; Pred. No. 4.2e-104; Mismatches 0; Indels 0; Gaps 0;				
Matches 432; Conservative 0; N.A.				
SEQUENCE FROM N.A.				
QY 1 MFRSDMPKNTAVENSL MTKQPSHSVSNSAPNQFRKP 60				
QY				
Db 1 MFRSDMPKNTAVENSL MTKQPSHSVSNSAPNQFRKP 60				
QY 61 RVRLTIGTRGGQSQTSDQGSLASLSPSRVAPRQDPLSSPPAGHTPEYRDTVIFDFPR 120				
QY				
Db 61 RVRLTIGTRGGQSQTSDQGSLASLSPSRVAPRQDPLSSPPAGHTPEYRDTVIFDFPR 120				
QY 121 LVSPLSREVEDAKPVKVERAPASEREGGEREVEDAKPVKVERAPASEREGGEREVEDAKPVKVERAPAS 180				
QY				
Db 121 LVSPLSREVEDAKPVKVERAPASEREGGEREVEDAKPVKVERAPASEREGGEREVEDAKPVKVERAPAS 180				
QY 181 ERGGEREVEDAKPVKVERAPASEREGGEREVEDAKPVKVERAPASEREGGEREVEDAKPVKVERAPAS 240				
QY				
Db 181 ERGGEREVEDAKPVKVERAPASEREGGEREVEDAKPVKVERAPASEREGGEREVEDAKPVKVERAPAS 240				
QY 241 ERGGEREVEDAKPVKVERAPASEREGGEREVEDAKPVKVERAPASEREGGEREVEDAKPVKVERAPAS 300				
QY				
Db 241 ERGGEREVEDAKPVKVERAPASEREGGEREVEDAKPVKVERAPASEREGGEREVEDAKPVKVERAPAS 300				
QY 301 ERGGEREVEDAKPVKVERAPASEREGGEREVEDAKPVKVERAPASEREGGEREVEDAKPVKVERAPAS 360				
QY				
Db 301 ERGGEREVEDAKPVKVERAPASEREGGEREVEDAKPVKVERAPASEREGGEREVEDAKPVKVERAPAS 360				
QY 361 ERGGEREVEDAKPVKVERAPASEREGGEREVEDAKPVKVERAPASEREGGEREVEDAKPVKVERAPAS 420				
QY				
Db 361 ERGGEREVEDAKPVKVERAPASEREGGEREVEDAKPVKVERAPASEREGGEREVEDAKPVKVERAPAS 420				
QY 421 VSNSAPNQFRKP 432				
QY				
Db 421 VSNSAPNQFRKP 432				
QY 421 VSNSAPNQFRKP 432				
QY				
Db 421 VSNSAPNQFRKP 432				

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OM protein - protein search, using SW model
Run on: January 28, 2005, 10:59:24 ; Search time 409.335 Seconds
378.592 Million cell updates/sec

Title: US-10-017-168-2
Perfect score: 2188
Sequence: 1 M E V R S D M P K N T A V E I S N L E H T R Q P S H S V S N S A P N Q F R K P 432

Scoring table: BLOSUM62
GapPen 10.0 , GapExt 0.5

Searched: 200273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23seqp04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003s:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	2188	100.0	432	AAB48316
2	1480	67.6	312	AAB48318
3	1048	47.9	232	AAB48317
4	268	12.2	4	AAB63397
5	255.5	11.7	567	AAB13147
6	254.5	11.6	1000	AQJ25647
7	249.5	11.4	522	AAB29778
8	245	11.2	1018	AAR98747
9	245	11.2	1018	AAR97039
10	245	11.2	1018	AAG66528
11	245	11.2	1018	ADJ95471
12	244.5	11.2	412	AQW03626
13	244.5	11.2	902	AAB29778
14	241	11.0	360	AQW03627
15	240.5	11.0	783	AQR05804
16	229	10.5	552	ADC31182
17	229	10.5	1388	AAB73896
18	225.5	10.3	1388	ADJ6333
19	224	10.2	845	ABN04814
20	223.5	10.2	864	ABM39026
21	216.5	9.9	489	ABBS8655
22	214.5	9.8	382	AAB02399
23	213.5	9.8	611	AAY29019
24	213.5	9.8	611	AAB25510
25	213.5	9.8	611	AQD17131

RESULT 1

ID AAB48316 standard; protein; 432 AA.

XX AAB48316;

XX AC

XX DT 11-SEP-2003 (revised)

XX DT 20-APR-2001 (first entry)

XX DE T. pallidum ssp. pallidum (Ni) acidic repeat protein (arp).

XX KW Treponema pallidum; acidic repeat protein; arp; immunogenic; syphilis; yaws; bejel.

XX OS Treponema pallidum; ssp. pallidum.

XX PN WO20077486-A2.

XX PD 21-DEC-2000.

XX PR 14-JUN-1999; 990US-0138981P.

XX PT (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PT Liu H, Steiner B, Rhodes B;

XX DR WPI; 2001-080711/09.

DR N-PSDB; AAC84647.

XX PT Detecting Treponema pallidum in blood, saliva, etc., by detecting formation of a complex between immunogenic peptides of acidic repeat protein of the bacterium and an antibody present in the biological sample.

PT Claim 15: FIG 6 ; 73pp; English.

XX PT The invention relates to a method of detecting presence of Treponema pallidum (TP), anti-treponemal antibodies (Abs), or both in a biological sample that involves contacting an acidic repeat protein (arp), or one or more isolated immunogenic TP peptides or arp with an Ab containing biological sample and then detecting the formation of a complex between immunogenic peptides and Ab. The presence of the complex indicates the presence of TP. The method is thus useful for diagnosing syphilis, yaws, and bejel diseases. The immunogenic peptides or the Ab raised against arp, as part of an immunogenic composition, are useful for inducing a protective immune response against syphilis, yaws or bejel caused by TP.

Adm05820 Human pro Apn46475 Thermococ Adi60170 Secreted Aae2398 Canine re Aae23036 Human thi Abp59691 Drosophil Abu20070 Protein e Aaw61247 Streptoco Abp54665 S. pneumo Ad45299 S. pneumo Abp56885 Staphyloc Av44506 Streptoco Abu1047 S. pneumo Abm92119 S. pneumo Abu43308 Protein e Abb63266 Drosophil Abb63269 Drosophil Abp56886 Staphyloc Ap40376 Sequence Apv20763 Human neu

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OM protein - protein search, using sw model
Run on: January 28, 2005, 11:12:20 ; Search time 17.5517 seconds
(without alignment)
655.635 Million cell updates/sec

Title: US-10-017-168-9
Perfect score: 101
Sequence: PKVVERASREGGEREVEDA 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues
Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02;*

1: uniprot_sprot;*
2: uniprot_trembl;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	101	100.0	256	2	083448	083448 treponema p
2	101	100.0	432	2	051953	051953 treponema p
3	101	100.0	548	2	093ca4	093ca4 treponema p
4	97	96.0	227	2	083449	083449 treponema p
5	97	96.0	348	2	09ALV7	09ALV7 treponema p
6	97	96.0	393	2	093ca3	093ca3 treponema p
7	97	96.0	428	2	09ALV6	09ALV6 treponema p
8	52	51.5	328	1	SWT16 SCHPO	SWT16 SCHPO
9	52	51.5	533	2	07Q186	07Q186 anopheles g
10	51	50.5	77	2	07XMT2	07XMT2 oryza sativ
11	50	49.5	166	2	09FBX0	09FBX0 arabidopsis
12	50	49.5	749	1	YU20_HUMAN	"Complete genome sequence of <i>Treponema pallidum</i> , the spirochete
13	49	48.5	699	2	0811Q9	0811Q9
14	49	48.5	719	2	025826	025826
15	48	47.5	226	2	09S2R0	09S2R0
16	48	47.5	482	2	092YV8	092YV8
17	48	47.5	491	2	092YY6	092YY6
18	48	47.5	723	2	07XG2	07XG2
19	47.5	723	2	094106	094106	
20	48	47.5	742	2	08P9B2	08P9B2
21	48	47.5	742	2	AJH60851	AJH60851
22	48	47.5	776	2	Q9JG99	Q9JG99
23	48	47.5	783	2	Q9JH64	Q9JH64
24	47	46.5	122	2	Q9KH4	Q9KH4
25	47	46.5	165	2	Q9IRC4	Q9IRC4
26	47	46.5	187	2	Q811JB	Q811JB
27	47	46.5	193	2	Q941T5	Q941T5
28	47	46.5	286	2	Q8QR05	Q8QR05
29	47	46.5	357	2	Q62AB0	Q62AB0
30	47	46.5	356	2	BAD03360	BAD03360
31	47	46.5	379	2	Q8mq44	Q8mq44

ALIGNMENTS

RESULT	1
ID	083448
AC	083448;
DT	01-NOV-1998 (TREMBLrel. 08, Created)
DT	01-NOV-1999 (TREMBLrel. 08, Last sequence update)
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE	Hypothetical protein TP0433;
GN	OrderdilocusName=TP0433;
OS	Treponema pallidum.
OC	Bacteria; Spirochaetes; Spirochaetaceae; Treponemata;
OX	NCBI_TaxID=160;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=Nichols;
RX	MEDLINE=98332770; PubMed=9665876;
RA	Dodson R.J., Gwynn M.L., Hickey B.K., Weinbstock G.M., White O., Sutton G.G., Ketchum K.A., Sodergren E., Hardham J.M., McLeod M.P., Clayton R.A., Ketchum K.A., Hodson R., Sodergren E., Hardham J.M., McLeod M.P., Salzberg S.L., Peterson J.D., Khalak H.G., Richardson D.L., Howell J.K., Chidambaram M., Utterback T.R., McDonald L.A., Artlach P., Bowman C., Cotton M.D., Fujii C., Garland S.A., Hatch B., Horst K., Roberts K.M., Sandusky M., Weidman J.F., Smith H.O., Venter J.C.;
RA	"Complete genome sequence of <i>Treponema pallidum</i> , the spirochete
RT	RT
RL	SEQUENCE FROM N.A.
EMBL	2811375-388 (1998); AE001220; AAC65421.1; -.
PIR	PIR; FT1326; FT1326.
DR	TP0433; -.
DR	Complete proteome; Hypothetical protein.
DR	SEQUENCE 256 AA; B90329D25A119E76 CRC64;
DR	Best Local Similarity 100.0%; Pred. No. 5.9e-07; Mismatches 0; Indels 0; Gaps 0;
DR	Matches 20; Conservative 0; Misaligned 0;
KW	Complete genome sequence of <i>Treponema pallidum</i> , the spirochete
SQ	Query Match 100.0%; Score 101; DB 2; Length 256;
QY	1 PKVVERASREGGEREVEDA 20
Db	1 PKVVERASREGGEREVEDA 208

Complete genome

RESULT	2
ID	051953
AC	051953;
DT	01-OCT-1998 (TREMBLrel. 06, Created)
DT	01-OCT-1998 (TREMBLrel. 06, Last sequence update)
DT	01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE	Acidic repeat protein.
OS	Treponema pallidum.
OC	Bacteria; Spirochaetes; Spirochaetaceae; Treponemata;
OX	NCBI_TaxID=160;
RN	[1]
RP	SEQUENCE FROM N.A.

Q34q45 caenorhabdil
Q9P3C3 neurophora
P34437 caenorhabdil
P10527 rattus norv
Q9yvz8 homo sapien
Q811C5 dirosophila
C86s86 homo sapien
Q8CG11 mus musculus
Q6Z4J3 mus musculus
Flac38029 mus musculus
Q9NvU0 homo sapien
Q96t23 homo sapien
Q33958 streptomyces
Q8nq53 corynebacter

OM protein - protein search, using sw model									
Run on: January 28, 2005, 10:59:24 ; Search time 18.9507 Seconds									
(without alignment) 378.592 Million cell updates/sec									
Searched: 2002273 seqs, 358729299 residues									
Total number of hits satisfying chosen parameters: 2002273									
Minimum DB seq length: 0									
Maximum DB seq length: 200000000									
Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries									
Database : A_Geneseq_23Sep04:*									
1: geneseqp1980b:*									
2: geneseqp1990b:*									
3: geneseqp2000b:*									
4: geneseqp2001b:*									
5: geneseqp2002b:*									
6: geneseqp2003ab:*									
7: geneseqp2004ab:*									
8: geneseqp2004ab:*									
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.									
SUMMARIES									
Result No.	Score	Query Length	DB ID	Description					ALIGNMENTS
1	101	100.0	20	AAB48321					
2	101	100.0	432	AAB48316	T. pallid				
3	97	96.0	232	AAB48317	Aab48316 T. pallid				
4	97	96.0	312	AAB48318	Aab48317 T. pallid				
5	85	84.2	21	AAB48325	Aab48318 T. pallid				
6	77	76.2	20	AAB48329	Aab48325 T. pallid				
7	77	76.2	20	AAB48328	Aab48326 T. pallid				
8	77	76.2	20	AAB48327	Aab48327 T. pallid				
9	67	66.3	20	AAB48320	Aab48320 T. pallid				
10	62	61.4	26	AAB48326	Aab48320 T. pallid				
11	58	57.4	20	AAB48330	Aab48330 T. pallid				
12	51	50.5	296	AAB48324	Aab48330 Novel hum				
13	50	49.5	133	AAB21773	Arabidopsis				
14	50	49.5	163	ADP83334	Adf83334 Human GRI				
15	50	49.5	166	ADG21772	Aag21772 Arabidopsis				
16	50	49.5	166	ADNT74723	Adn74723 Thale cre				
17	50	49.5	749	ADM78419	Adm78419 Human pro				
18	50	49.5	749	ADB95780	Ab95780 Human pro				
19	50	49.5	749	ADP83330	Adf83330 Human GRI				
20	50	49.5	749	ADP83330	Adf83330 Human GRI				
21	50	49.5	754	ADB20997	Aab20997 Human nuc				
22	50	49.5	757	ADM79103	Adm79103 Human pro				
23	50	49.5	790	AAB41603	Aab41603 Human ORP				
24	48	47.5	888	AABP731624	Abp731624 Candia a				
25	47	45	69	AABP731624	Abp731624 Candia a				
26	47	45	69	AABP731624	Abp731624 Candia a				
27	47	45	69	AABP731624	Abp731624 Candia a				
28	47	45	69	AABP731624	Abp731624 Candia a				
29	47	45	69	AABP731624	Abp731624 Candia a				
30	47	45	69	AABP731624	Abp731624 Candia a				
31	47	45	69	AABP731624	Abp731624 Candia a				
32	47	45	69	AABP731624	Abp731624 Candia a				
33	47	45	69	AABP731624	Abp731624 Candia a				
34	47	45	69	AABP731624	Abp731624 Candia a				
35	47	45	69	AABP731624	Abp731624 Candia a				
36	47	45	69	AABP731624	Abp731624 Candia a				
37	47	45	69	AABP731624	Abp731624 Candia a				
38	47	45	69	AABP731624	Abp731624 Candia a				
39	47	45	69	AABP731624	Abp731624 Candia a				
40	47	45	69	AABP731624	Abp731624 Candia a				
41	47	45	69	AABP731624	Abp731624 Candia a				
42	47	45	69	AABP731624	Abp731624 Candia a				
43	47	45	69	AABP731624	Abp731624 Candia a				
44	47	45	69	AABP731624	Abp731624 Candia a				
45	47	45	69	AABP731624	Abp731624 Candia a				
46	47	45	69	AABP731624	Abp731624 Candia a				
47	47	45	69	AABP731624	Abp731624 Candia a				
48	47	45	69	AABP731624	Abp731624 Candia a				
49	47	45	69	AABP731624	Abp731624 Candia a				
50	47	45	69	AABP731624	Abp731624 Candia a				
51	47	45	69	AABP731624	Abp731624 Candia a				
52	47	45	69	AABP731624	Abp731624 Candia a				
53	47	45	69	AABP731624	Abp731624 Candia a				
54	47	45	69	AABP731624	Abp731624 Candia a				
55	47	45	69	AABP731624	Abp731624 Candia a				
56	47	45	69	AABP731624	Abp731624 Candia a				
57	47	45	69	AABP731624	Abp731624 Candia a				
58	47	45	69	AABP731624	Abp731624 Candia a				
59	47	45	69	AABP731624	Abp731624 Candia a				
60	47	45	69	AABP731624	Abp731624 Candia a				
61	47	45	69	AABP731624	Abp731624 Candia a				
62	47	45	69	AABP731624	Abp731624 Candia a				
63	47	45	69	AABP731624	Abp731624 Candia a				
64	47	45	69	AABP731624	Abp731624 Candia a				
65	47	45	69	AABP731624	Abp731624 Candia a				
66	47	45	69	AABP731624	Abp731624 Candia a				
67	47	45	69	AABP731624	Abp731624 Candia a				
68	47	45	69	AABP731624	Abp731624 Candia a				
69	47	45	69	AABP731624	Abp731624 Candia a				
70	47	45	69	AABP731624	Abp731624 Candia a				
71	47	45	69	AABP731624	Abp731624 Candia a				
72	47	45	69	AABP731624	Abp731624 Candia a				
73	47	45	69	AABP731624	Abp731624 Candia a				
74	47	45	69	AABP731624	Abp731624 Candia a				
75	47	45	69	AABP731624	Abp731624 Candia a				
76	47	45	69	AABP731624	Abp731624 Candia a				
77	47	45	69	AABP731624	Abp731624 Candia a				
78	47	45	69	AABP731624	Abp731624 Candia a				
79	47	45	69	AABP731624	Abp731624 Candia a				
80	47	45	69	AABP731624	Abp731624 Candia a				
81	47	45	69	AABP731624	Abp731624 Candia a				
82	47	45	69	AABP731624	Abp731624 Candia a				
83	47	45	69	AABP731624	Abp731624 Candia a				
84	47	45	69	AABP731624	Abp731624 Candia a				
85	47	45	69	AABP731624	Abp731624 Candia a				
86	47	45	69	AABP731624	Abp731624 Candia a				
87	47	45	69	AABP731624	Abp731624 Candia a				
88	47	45	69	AABP731624	Abp731624 Candia a				
89	47	45	69	AABP731624	Abp731624 Candia a				
90	47	45	69	AABP731624	Abp731624 Candia a				
91	47	45	69	AABP731624	Abp731624 Candia a				
92	47	45	69	AABP731624	Abp731624 Candia a				
93	47	45	69	AABP731624	Abp731624 Candia a				
94	47	45	69	AABP731624	Abp731624 Candia a				
95	47	45	69	AABP731624	Abp731624 Candia a				
96	47	45	69	AABP731624	Abp731624 Candia a				
97	47	45	69	AABP731624	Abp731624 Candia a				
98	47	45	69	AABP731624	Abp731624 Candia a				
99	47	45	69	AABP731624	Abp731624 Candia a				
100	47	45	69	AABP731624	Abp731624 Candia a				
101	47	45	69	AABP731624	Abp731624 Candia a				
102	47	45	69	AABP731624	Abp731624 Candia a				
103	47	45	69	AABP731624	Abp731624 Candia a				
104	47	45	69	AABP731624	Abp731624 Candia a				
105	47	45	69	AABP731624	Abp731624 Candia a				
106	47	45	69	AABP731624	Abp731624 Candia a				
107	47	45	69	AABP731624	Abp731624 Candia a				
108	47	45	69	AABP731624	Abp731624 Candia a				
109	47	45	69	AABP731624	Abp731624 Candia a				
110	47	45	69	AABP731624	Abp731624 Candia a				
111	47	45	69	AABP731624	Abp731624 Candia a				
112	47	45	69	AABP731624	Abp731624 Candia a				
113	47	45	69	AABP731624	Abp731624 Candia a				
114	47	45	69	AABP731624	Abp731624 Candia a				
115	47	45	69	AABP731624	Abp731624 Candia a				
116	47	45	69	AABP731624	Abp731624 Candia a				
117	47	45	69	AABP731624	Abp731624 Candia a				
118	47	45	69	AABP731624	Abp731624 Candia a				
119	47	45	69	AABP731624	Abp731624 Candia a				
120	47	45	69	AABP731624	Abp731624 Candia a				
121	47	45	69	AABP731624	Abp731624 Candia a				
122	47	45	69	AABP731624	Abp731624 Candia a				
123	47	45	69	AABP731624	Abp731624 Candia a				
124	47	45	69	AABP731624	Abp731624 Candia a				
125	47	45	69	AABP731624	Abp731624 Candia a				
126	47	45	69	AABP731624	Abp731624 Candia a				
127	47	45	69	AABP731624	Abp731624 Candia a				
128	47	45	69	AABP731624	Abp731624 Candia a				
129	47	45	69	AABP731624	Abp731624 Candia a				
130	47	45	69	AABP731624	Abp731624 Candia a				
131	47	45	69	AABP731624	Abp731624 Candia a				
132	47	45	69	AABP731624	Abp731624 Candia a				

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OM protein - protein search, using sw model

Title: US-10-017-168-11

Run on: January 28, 2005, 11:05:24 ; Search time 3.89507 Seconds

Sequence: 1 GHAGIPGLVSLAPAAAQLGIGIVY 25

Scoring table: BLOSUM62

Gapext 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_794*

1: piri:*

2: piri:*

3: piri:*

4: piri:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Length DB ID Description

Result No.	Score	Query	Length	DB ID	Description
1	124	100.0	256	2 F71326	hypothetical protein tp0413 - syphilis spirochete
2	56.5	45.6	747	1 EABO	C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete) C:Date: 24-Jul-1998 #Sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
3	55	44.4	272	2 F87351	C:Accession: F71326
4	53.5	43.1	242	2 T34951	R;Fraser, C.M.; Morris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Fraser, C.M.; Morris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Fraser, J.; Kralak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
5	53.5	43.1	347	2 T35013	Science 281, 375-388, 1998
6	53	42.7	770	2 S59623	A;Title: Complete genome sequence of <i>Treponema pallidum</i> , the syphilis spirochete.
7	52.5	42.3	860	1 EAMS	A;Reference number: A71250; MUID:98332770; PMID:9665876
8	50.5	40.7	767	1 A35645	A;Accession: F71326
9	50	40.3	668	2 F83287	A;Status: preliminary; nucleic acid sequence not shown; translation not shown
10	50	40.3	792	1 EABO	A;Molecule type: DNA
11	49.9	39.9	377	2 F95948	A;Residues: 1-255 <COL>
12	49.5	39.9	434	2 S04534	A;Cross-references: UNIPROT:083448; GB:AE001220; GB:AE000520; NID:93322705; PIDN:AA
13	49	39.5	1053	2 C97826	A;Experimental source: strain Nichols
14	49	39.5	349	2 T44856	C:Generics:
15	49	39.5	400	2 H83353	A;Gene: TP0433
16	49	39.5	459	2 JC7931	RESULT 2
17	49	39.5	603	2 S34130	elastin precursor, splice form a - bovine
18	49	39.5	1053	2 B70987	N;Alternate names: tropoelastin
19	48.5	39.1	320	2 F82763	N;Contains: elastin precursor, splice form b; elastin precursor, splice form c
20	48.5	39.1	542	2 AB3057	C:Species: Bos primigenius taurus (cattle)
21	48.5	39.1	567	2 A96229	C:Date: 08-Jun-1989 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
22	48.5	39.1	864	1 EART	C:Accession: A31865; A26728; B65728; C26728; A22313; I5886
23	48	38.7	181	2 S38907	R;Yeh, H.; Anderson, N.; Ornstein-Goldstein, N.; Bashir, M.M.; Rosenblum, J.C.; Ab
24	48	38.7	195	2 S32123	Biochemistry 28, 2365-2370, 1989
25	48	38.7	202	2 B87342	A;Title: Structure of the bovine elastin gene and S1 nuclease analysis of alternative splicing
26	48	38.7	334	2 F86462	A;Reference number: A31865; MUID:89274159; PMID:2543440
27	48	38.7	363	2 T34631	A;Accession: A31865
28	48	38.7	421	2 A26691	A;Molecule type: DNA
29	48	38.7	522	2 T31310	A;Residues: 1-27 <YEH>

ALIGNMENTS

30	48	38.7	784	2 A26601	elastin precursor
31	47.5	38.3	441	2 A92642	hypothetical protein
32	47	37.9	290	2 B87679	integral membrane
33	47	37.9	296	2 I40328	serum-resistance P
34	47	37.9	387	2 T44873	probable secreted
35	47	37.9	464	2 A81480	PTS system, fructo
36	47	37.9	464	2 AG119	olid protein [impo
37	47	37.9	614	2 D87410	potassium/proton a
38	47	37.9	619	2 A13336	precorin-3 methyl
39	46.5	37.5	245	2 T03534	conserved hypotet
40	46.5	37.5	355	2 H90245	formaldehyde dehyd
41	46.5	37.5	399	2 A55777	probable glycosyla
42	46.5	37.5	476	2 F93286	hypothetical prote
43	46.5	37.5	511	2 D97965	sugar ABC transpor
44	46.5	37.5	511	2 H95097	phosphoglucomutase
45	46.5	37.5	566	2 A93487	

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On protein - protein search, using bw model

Run on:

January 28, 2005, 10:59:24 ; Search time 23.6884 seconds

(without alignments)

378.592 Million cell updates/sec

Title: US-10-017-168-11

Perfect score: 124

Sequence: 1 GHAGIPGLUVSLAPAAAQOLGIVY 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 200273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 200273

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A_Geneseq_23Seq04:*

1: geneseqp19808:*

2: geneseqp19808:*

3: geneseqp20008:*

4: geneseqp20018:*

5: geneseqp20028:*

6: geneseqp20038:*

7: geneseqp20038:*

8: geneseqp20048:*

Pred. No. 18 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

#	Query	Match Length	DB ID	Description
1	124	100.0	25	AAB48323
2	124	100.0	232	Aab48317
3	124	100.0	312	Aab48318
4	124	100.0	432	Aab48316
5	60	48.4	1257	Abo68544
6	59	48.5	843	Abo68024
7	54	44.0	1133	Abo83385
8	51	41.1	28	AAB15028
9	51	41.1	283	AAG12779
10	51	41.1	306	AAG12778
11	51	41.1	340	AAG12777
12	51	41.1	352	Abo65983
13	51	41.1	437	Ab074993
14	50.5	40.7	593	AAB08404
15	50.5	40.7	652	AAB08403
16	50.5	40.7	767	AAB07599
17	50.5	40.7	767	AAB08401
18	50	40.3	147	AAB01304
19	50	40.3	171	AAY69137
20	50	40.3	183	AAY01311
21	50	40.3	183	AAY69133
22	50	40.3	200	AAY01305
23	50	40.3	216	AAY01310
24	50	40.3	421	Abo70994
25	50	40.3	472	AAB88422

Maximum Match 0%
 Listing first 45 summaries

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A_Geneseq_23Seq04:*

1: geneseqp19808:*

2: geneseqp19808:*

3: geneseqp20008:*

4: geneseqp20018:*

5: geneseqp20028:*

6: geneseqp20038:*

7: geneseqp20038:*

8: geneseqp20048:*

Database : A_Geneseq_23Seq04:*

1: geneseqp19808:*

2: geneseqp19808:*

3: geneseqp20008:*

4: geneseqp20018:*

5: geneseqp20028:*

6: geneseqp20038:*

7: geneseqp20038:*

8: geneseqp20048:*

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A_Geneseq_23Seq04:*

1: geneseqp19808:*

2: geneseqp19808:*

3: geneseqp20008:*

4: geneseqp20018:*

5: geneseqp20028:*

6: geneseqp20038:*

7: geneseqp20038:*

8: geneseqp20048:*

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A_Geneseq_23Seq04:*

1: geneseqp19808:*

2: geneseqp19808:*

3: geneseqp20008:*

4: geneseqp20018:*

5: geneseqp20028:*

6: geneseqp20038:*

7: geneseqp20038:*

8: geneseqp20048:*

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A_Geneseq_23Seq04:*

1: geneseqp19808:*

2: geneseqp19808:*

3: geneseqp20008:*

4: geneseqp20018:*

5: geneseqp20028:*

6: geneseqp20038:*

7: geneseqp20038:*

8: geneseqp20048:*

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A_Geneseq_23Seq04:*

1: geneseqp19808:*

2: geneseqp19808:*

3: geneseqp20008:*

4: geneseqp20018:*

5: geneseqp20028:*

6: geneseqp20038:*

7: geneseqp20038:*

8: geneseqp20048:*

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A_Geneseq_23Seq04:*

1: geneseqp19808:*

2: geneseqp19808:*

3: geneseqp20008:*

4: geneseqp20018:*

5: geneseqp20028:*

6: geneseqp20038:*

7: geneseqp20038:*

8: geneseqp20048:*

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A_Geneseq_23Seq04:*

1: geneseqp19808:*

2: geneseqp19808:*

3: geneseqp20008:*

4: geneseqp20018:*

5: geneseqp20028:*

6: geneseqp20038:*

7: geneseqp20038:*

8: geneseqp20048:*

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A_Geneseq_23Seq04:*

1: geneseqp19808:*

2: geneseqp19808:*

3: geneseqp20008:*

4: geneseqp20018:*

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7: geneseqp20038:*

8: geneseqp20048:*

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A_Geneseq_23Seq04:*

1: geneseqp19808:*

2: geneseqp19808:*

3: geneseqp20008:*

4: geneseqp20018:*

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6: geneseqp20038:*

7: geneseqp20038:*

8: geneseqp20048:*

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A_Geneseq_23Seq04:*

1: geneseqp19808:*

2: geneseqp19808:*

3: geneseqp20008:*

4: geneseqp20018:*

5: geneseqp20028:*

6: geneseqp20038:*

7: geneseqp20038:*

8: geneseqp20048:*

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A_Geneseq_23Seq04:*

1: geneseqp19808:*

2: geneseqp19808:*

3: geneseqp20008:*

4: geneseqp20018:*

5: geneseqp20028:*

6: geneseqp20038:*

7: geneseqp20038:*

8: geneseqp20048:*

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A_Geneseq_23Seq04:*

1: geneseqp19808:*

2: geneseqp19808:*

3: geneseqp20008:*

4: geneseqp20018:*

5: geneseqp20028:*

6: geneseqp20038:*

7: geneseqp20038:*

8: geneseqp20048:*

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A_Geneseq_23Seq04:*

1: geneseqp19808:*

2: geneseqp19808:*

3: geneseqp20008:*

4: geneseqp20018:*

5: geneseqp20028:*

6: geneseqp20038:*

7: geneseqp20038:*

8: geneseqp20048:*

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A_Geneseq_23Seq04:*

1: geneseqp19808:*

2: geneseqp19808:*

3: geneseqp20008:*

4: geneseqp20018:*

5: geneseqp20028:*

6: geneseqp20038:*

7: geneseqp20038:*

8: geneseqp20048:*

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A_Geneseq_23Seq04:*

1: geneseqp19808:*

2: geneseqp19808:*

3: geneseqp20008:*

4: geneseqp20018:*

5: geneseqp20028:*

6: geneseqp20038:*

7: geneseqp20038:*

8: geneseqp20048:*

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A_Geneseq_23Seq04:*

1: geneseqp19808:*

2: geneseqp19808:*

3: geneseqp20008:*

4: geneseqp20018:*

5: geneseqp20028:*

6: geneseqp20038:*

7: geneseqp20038:*

8: geneseqp20048:*

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A_Geneseq_23Seq04:*

1: geneseqp19808:*

2: geneseqp19808:*

3: geneseqp20008:*

4: geneseqp20018:*

5: geneseqp20028:*

6: geneseqp20038:*

7: geneseqp20038:*

8: geneseqp20048:*

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A_Geneseq_23Seq04:*

1: geneseqp19808:*

2: geneseqp19808:*

3: geneseqp20008:*

4: geneseqp20018:*

5: geneseqp20028:*

6: geneseqp20038:*

7: geneseqp20038:*

8: geneseqp20048:*

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A_Geneseq_23Seq04:*

1: geneseqp19808:*

2: geneseqp19808:*

3: geneseq

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On protein - protein search, using sw model

Run on: January 28, 2005, 11:05:24 ; Search time 3.89507 Seconds
 (without alignments) 617.555 Million cell updates/sec

Title: US-10-017-168-12
 Perfect score: 137
 Sequence: 1 VPARPQDRPLSSPPAGHTVPEYRD 25

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. 18 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Length DB ID

1 137 100.0 256 2 F71326

hypothetical protein
 hypothetical prote
 hypothetical prote
 probable membrane
 translation elonga
 hypothetical prote
 hypothetical prote
 probable cell-adhe
 RING1/Y protein - g

2 60 43.8 97 2 G70866

hypothetical prote
 hypothetical prote
 probable membrane
 translation elonga
 hypothetical prote
 hypothetical prote
 probable cell-adhe

3 52 38.0 212 2 C72464

hypothetical prote
 probable membrane
 translation elonga
 hypothetical prote
 hypothetical prote
 probable cell-adhe

4 52 38.0 622 2 S56214

hypothetical prote
 probable membrane
 translation elonga
 hypothetical prote
 hypothetical prote
 probable cell-adhe

5 37.2 982 2 S09810

hypothetical prote
 probable cell-adhe

6 37.2 1192 2 T17255

hypothetical prote
 probable cell-adhe

7 51 37.2 2 T18543

hypothetical prote
 probable cell-adhe

8 50 36.5 197 2 S37948

hypothetical prote
 probable cell-adhe

9 50 36.5 417 2 T22024

hypothetical prote
 probable cell-adhe

10 50 36.5 827 2 AC2963

hypothetical prote
 probable cell-adhe

11 50 36.5 881 2 B98320

hypothetical prote
 probable cell-adhe

12 50 36.5 1057 2 T04874

hypothetical prote
 probable cell-adhe

13 50 36.5 1102 2 T28666

hypothetical prote
 probable cell-adhe

14 50 36.5 6420 2 T30283

hypothetical prote
 probable cell-adhe

15 49 35.8 173 2 B39141

hypothetical prote
 probable cell-adhe

16 49 35.8 396 1 JH0333

hypothetical prote
 probable cell-adhe

17 49 35.8 718 1 TNBFB6

hypothetical prote
 probable cell-adhe

18 49 35.8 760 2 T02957

hypothetical prote
 probable cell-adhe

19 49 35.8 900 2 B87220

hypothetical prote
 probable cell-adhe

20 49 35.8 948 2 T26417

hypothetical prote
 probable cell-adhe

21 49 35.8 2115 2 S38080

hypothetical prote
 probable cell-adhe

22 49 35.8 2205 1 MNWWRN

hypothetical prote
 probable cell-adhe

23 49 35.8 101 2 D83375

hypothetical prote
 probable cell-adhe

24 48 35.0 132 2 A75491

hypothetical prote
 probable cell-adhe

25 48 35.0 333 2 H87220

hypothetical prote
 probable cell-adhe

26 48 35.0 443 2 A38219

hypothetical prote
 probable cell-adhe

27 48 35.0 499 2 CPHS

hypothetical prote
 probable cell-adhe

28 48 35.0 510 1 S43516

ALIGNMENTS

RESULT 1

F71326 hypothetical protein TP0433 - syphilis spirochete

C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)

C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004

C;Accession: F71326 R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gw

erson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; Mc

they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.

Science 261, 375-383, 1998

A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.

A;Reference number: A71250; MID:98332770; PMID:9665876

A;Accession: F71326 A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA A;Residues: 1-256 <COL>

A;Cross-references: UNIPROT:083448; GB:AE001220; GB:AB000520; NID:g3322705; PIDN: AAC65 A;Experimental source: strain Nichols C;Genetics: A;Gene: T0433

Query Match Similarity 100.0%; Score 137; DB 2; Length 256; Best Local Similarity 100.0%; Pred No. 5.3e-11; Matches 25; Conservative 0; Mismatches 0; Intels 0; Gaps 0; Ov 1 VPARPQDRPLSSPPAGHTVPEYRD 25 Db 144 VPARPQDRPLSSPPAGHTVPEYRD 168

protein kinase (EC 2.7.11.1)
 hypothetical prote
 alpha-2 macroglobu
 Bassoon protein -
 con 8 protein - Ne
 env polyprotein, r
 hypothetical 36.9k
 hypothetical prote
 retrovirus-related
 hypothetical prote
 probable kinase/ph
 extein-like prote
 conserved hypothet
 ribonucleoprotein,
 hypothetical prote
 probable lipoprote

30	48	35.0	819	2	A53714
31	48	35.0	1171	2	T35548
32	48	35.0	1476	2	A41185
33	48	35.0	3942	2	T42730
34	47.5	34.7	176	2	S02210
35	47.5	34.7	312	2	B29350
36	47.5	34.7	336	2	JC4102
37	47.5	34.7	405	2	E70545
38	47.5	34.7	445	2	C47757
39	47.5	34.7	674	2	T23235
40	47.5	34.7	725	2	T35114
41	47.5	34.7	1188	2	S49915
42	47	34.3	317	2	E75421
43	47	34.3	324	2	S12111
44	47	34.3	328	2	T01944
45	47	34.3	358	2	F70577

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On protein - protein search, using bw model

Run on: January 28, 2005, 10:59:24 ; Search time 23.6884 Seconds
(without alignments)

378.592 Million cell updates/sec

Title: US-10-017-168-12

Perfect score: 137

Sequence: 1 VPAPRQDRPLSSPPAGHTVPEYRD 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 200273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters:

200273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_GenSeq_23Sep04;*

- 1: geneseq23Sep04;*
- 2: geneseq1980s;*
- 3: geneseq2008;*
- 4: geneseq2001a;*
- 5: geneseq2002a;*
- 6: geneseq2003a;*
- 7: geneseq2003b;*
- 8: geneseq2004b;*

Pred. No. 1 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description	ALIGNMENTS
1	137	100.0	25	4	AAB48324	RESULT 1
2	137	100.0	232	4	AAB48317	AAB48324, standard; peptide; 25 AA.
3	137	100.0	312	4	AAB48318	XX
4	137	100.0	432	4	AAB48316	XX
5	59.5	43.4	325	7	ABO77834	20-APR-2001 (first entry)
6	59.5	42.0	476	4	ABG13460	T. pallidum acidic repeat protein immunogenic peptide arp 6.
7	57.5	42.0	476	6	ABO00838	XX
8	57	41.6	126	4	AMM2113	XX
9	57	41.6	322	4	AMM0075	XX
10	57	41.6	362	4	ABG03440	XX
11	57	41.6	387	4	ABG27023	XX
12	57	41.6	491	2	ABW2316	XX
13	57	41.6	647	7	ADD67649	XX
14	57	41.6	647	7	ADD67647	XX
15	57	41.6	989	6	ABU21195	The invention relates to a method of detecting presence of Treponema pallidum (TP), anti-treponemal antibodies (Ab), or both in a biological sample that involves contacting an acidic repeat protein (arp), or one or more isolated immunogenic TP peptides of arp with an Ab containing immunogenic peptides and Ab. The presence of the complex indicates the presence of TP. The method is thus useful for diagnosing syphilis, yaws, and bejel diseases. The immunogenic peptides or the Abs raised against arp, as part of an immunogenic composition, are useful for inducing a protective immune response against syphilis, yaws or bejel caused by TP.
16	57	41.6	1370	6	ABJ19769	CC
17	57	41.6	1270	7	ADD67643	CC
18	57	41.6	1270	7	ADD67648	CC
19	57	41.6	1338	7	ABD0104	CC
20	56	40.9	147	4	AAQ02546	CC
21	56	40.9	444	6	AAU52218	CC
22	56	40.9	444	6	ABM48737	CC
23	55.5	40.5	614	7	ABO11464	CC
24	55.5	40.5	2768	4	ABH68397	CC
25	40.1	455	4	ABH43987	CC	

Run on:	January 28, 2005, 11:12:20	(Search time 18.4293 Seconds (without alignments) 655.635 Million cell updates/sec
OM protein - protein search, using SW model		
Title:	US-10-017-168-13	
Perfect score:	105	
Sequence:	1 VVEPASEREGGEREVEVDPKV 21	
Scoring table:	BLOSUM62	
Gapop:	10.0	, Gapext 0.5
Searched:	1825181 seqs, 515374646 residues	
Total number of hits satisfying chosen parameters:	1825181	
Minimum DB seq. length:	0	
Maximum DB seq. length:	200000000	
Post-processing:	Minimum Match 0%	
	Maximum Match 100%	
Database:	UniProt 02-* 1: uniprot_sprot: 2: uniprot_trembl: [1]	
Pred. No. 18 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.		
		SUMMARIES
Result No.	Score	Query Match Length DB ID Description
1	105	100.0 256 2 083448 083448 treponema p
2	105	100.0 348 2 09ALV7 09ALV7 treponema p
3	105	100.0 393 2 093CA3 093CA3 treponema p
4	105	100.0 428 2 09ALV6 09ALV6 treponema p
5	105	100.0 432 2 051953 051953 treponema p
6	105	100.0 548 2 093CA4 093CA4 treponema p
7	98	93.3 227 2 083449 083449 treponema p
8	56	53.3 2 07038 07038 1 TRIO_HUMAN
9	55	52.4 3038 1 TRIO_HUMAN
10	53	50.5 449 2 09LS16 09LS16 arachidopsis
11	52	49.5 543 2 094334 094334 arachidopsis
12	52	49.5 558 2 09SY77 09SY77 arachidopsis
13	51	48.6 362 2 06JE13 06JE13 pitchia memb
14	51	48.6 362 2 AAU12523 AAU12523 pitchia me
15	51	48.6 1372 2 09VM46 09VM46 drosophila
16	51	48.6 1372 2 08PSX9 08PSX9 drosophila
17	50	47.6 183 2 Q6N885 Q6N885 rhodopseudo
18	50	47.6 183 2 CAE88537 CAE88537 rhodopseudo
19	50	47.6 474 2 Q97Y15 Q97Y15 bifidobacter
20	50	47.6 585 2 Q9FN0 Q9FN0 streptomyce
21	50	47.6 699 2 Q81Q90 Q81Q90 plasmodium
22	50	47.6 719 2 Q25Q26 Q25Q26 plasmodium
23	49	46.7 471 2 Q81ZP7 Q81ZP7 homo sapien
24	49	46.7 1135 2 Q7MB2 Q7MB2 porphyromon
25	48.5	46.2 328 1 SWI6_SC9PO SWI6_SC9PO schizosacchar
26	48	45.7 154 2 Q39814 Q39814 glycine max
27	48	45.7 226 2 Q8SR0 Q8SR0 oryza sativ
28	48	45.7 650 2 Q6DDE9 Q6DDE9 xenopus lae
29	48	45.7 652 2 Q8TWL1 Q8TWL1 methanoplu
30	48	45.7 723 2 Q7XG32 Q7XG32 oryza sativ
31	48	45.7 723 2 Q94106 Q94106 oryza sativ
		RESULT 1
RP	083448	SEQUENCE FROM N.A.
RC	083448	PRELIMINARY; PRT; 256 AA.
RX	083448;	MEDLINE=9332770; PubMed=9665876;
RA	01-NOV-1998 (TREMBL); 08, Created)	
DT	01-NOV-1998 (TREMBL); 08, Last sequence update)	
DT	01-JUN-2003 (TREMBL); 24, Last annotation update)	
DE	Hypothetical protein TP0433.	
DN	OrderedLocusNames=TP0433;	
OS	Treponema pallidum.	
OC	Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.	
OX	NCBI_TaxId=160;	
RN	[1]	
		ALIGNMENTS
RESULT 2		
ID	09ALV7	PRELIMINARY; PRT; 348 AA.
AC	09ALV7;	
DT	01-JUN-2001 (TREMBL); 17, Created)	
DT	01-DEC-2001 (TREMBL); 19, Last sequence update)	
DT	01-OCT-2002 (TREMBL); 22, Last annotation update)	
DE	Acidic repeat protein.	
GN	Name=arp;	
OS	Treponema pallidum (subsp. pertenue) (Yaws treponeme).	
OC	Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.	
OX	NCBI_TaxId=168;	
RN	[1]	

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OM protein - protein search, using sw model

Run on: January 28, 2005, 10:59:24 ; Search time 19.8983 Seconds

{without alignments} updates/sec 378.592 Million cell

Title: US-10-017-168-13
Perfect score: 105
Sequence: VVERPASEREGGEREVEDVPKV 21

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 200273 seqs, 35872999 residues

Total number of hits satisfying chosen parameters: 200273

Minimum DB seq length: 0
Maximum DB seq length: 0

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Seqp04:*

1: geneseq_1980s:*

2: geneseqp1980s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	105	100.0	21	4 AAB48325
2	105	100.0	232	4 AAB48317
3	105	100.0	312	4 AAB48318
4	105	100.0	432	4 AAB48316
5	85	81.0	20	4 AAB48321
6	65	61.9	20	4 AAB48329
7	65	61.9	20	4 AAB48328
8	65	61.9	20	4 AAB48327
9	62	59.0	26	4 AAB48326
10	55	52.4	20	4 AAB48320
11	55	52.4	2980	4 ABG20755
12	55	52.4	3038	4 ABG17025
13	55	52.4	3038	6 ABO07225
14	55	52.4	3038	6 ABO07226
15	55	52.4	3060	4 ABG06311
16	53	50.5	20	4 AAB48330
17	53	49.9	5	ABG93640
18	51	48.6	1167	5 ABB5757
19	49	46.7	121	7 ADT60314
20	49	46.7	216	7 ADP58964
21	49	46.7	471	6 AAO26110
22	49	46.7	472	6 ADT72050
23	49	46.7	472	8 ADT72052
24	49	46.7	472	8 ADT72058
25	49	46.7	944	8 ADI16666

Maximum Match 0%
Listing first 45 summaries

RESULT 1
ID AAB48325 standard; peptide; 21 AA.
XX

AC

AAB48325;

XX

DT

20-APR-2001 (first entry)

XX

DE

T. pallidum acidic repeat protein immunogenic peptide arp 7.

XX

KW

Treponema pallidum; acidic repeat protein; arp; immunogenic; syphilis;

XX

yaws; bejel.

XX

OS

Treponema pallidum.

XX

PN

WO2007486-A2.

XX

PD

21-DEC-2000.

XX

PP

14-JUN-1999; 99US0-0138981P.

XX

PA

(USSH) US DEPT HEALTH & HUMAN SERVICES.

XX

PI

Liu H, Steiner B, Rhodes B;

XX

DR

WPI; 2001-080711/09.

XX

PT

Detecting Treponema pallidum in blood, saliva, etc., by detecting

XX

PT

formation of a complex between immunogenic peptides of acidic repeat

XX

PT

protein of the bacterium and an antibody present in the biological

sample.

XX

PS

Claim 15; Fig 11; 73pp; English.

XX

CC

The invention relates to a method of detecting presence of Treponema

XX

CC

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OM protein - protein Search, using SW model
Run on: January 28, 2005, 11:05:24 ; Search time 4.05087 Seconds
Sequence: 1 VWE PASHEGGEREV ASQHTKOPSHS 26

Title: US-10-017-168-14
Perfect score: 137
Sequence: 1 VWE PASHEGGEREV ASQHTKOPSHS 26
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0*
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79: *
1: pix1: *
2: pix2: *
3: pix3: *
4: pix4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	137	100.0	227	2	G71326 hypothetical protein TP0434 - syphilis spirochete
2	62	45.3	256	2	F771326 hypothetical prote
3	52	38.0	303	2	B83367 probable glycosyl
4	52	38.0	203114	2	probable protein -
5	49.5	36.1	2722	2	T20532 hypothetical prote
6	49.5	36.1	2738	2	E88320 protein F07A11_6 !
7	49	35.8	551	2	H69371 probable acid-CoA
8	49	35.8	555	2	D71298 probable uridine k
9	49	35.8	2649	2	T51023 hypothetical prote
10	48	35.0	546	1	S71008 propionyl-CoA carb
11	48	35.0	723	2	conserved hypothet
12	47	34.3	445	2	hypothetical prote
13	47	34.3	467	2	hypothetical prote
14	47	34.3	1154	2	protein P1K21_24
15	47	34.3	1236	2	regulator protein
16	45.5	33.9	161	2	T50904 Mg protoporphyrin
17	46.5	33.9	519	2	conserved hypothet
18	46.5	33.9	695	2	transketolase (EC
19	46	33.6	510	2	amphiphysin (clone
20	46	33.6	510	2	probable propionyl
21	46	33.6	707	2	propionyl-CoA carb
22	46	33.6	1034	2	probable RNA helic
23	45.5	33.2	277	2	integrin alpha-VC
24	45.5	33.2	813	2	hypothetical prote
25	45.5	33.2	1280	2	hypothetical prote
26	45	32.8	184	2	probable Yfe4CD1
27	45	32.8	330	2	pseudouridylate sy
28	45	32.8	343	2	hypothetical prote
29	45	32.8	45	1	GTP cyclohydrolase
30					

ALIGNMENTS

RESULT 1
G71326 hypothetical protein TP0434 - syphilis spirochete
C.Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C.Date: 24-Jul-1998 #Sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C.Accession: G71326
R.Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodaon, R.; Gwilymson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McElroy, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A.Title: Complete genome sequence of *Treponema pallidum*, the syphilis spirochete.
A.Reference number: A71250; MUID:98332770; PMID:9665876
A.Accession: G71326
A.Status: preliminary; nucleic acid sequence not shown; translation not shown
A.Molecule type: DNA
A.Residues: 1-227 <CDS>
A.Cross-references: UNIPROT:OB3448; GB:AB001220; GB:AE000520; NID:93322705; PIDN: AAC654
A.Experimental source: strain Nichols
A.Genetics: C;Genetics:
A.Gene: Tp0434
Query Match 100.0%; Score 137; DB 2; Length 227;
Best Local Similarity 100.0%; Pred. No. 8.4e-13; Mismatches 0; Indels 0; Gaps 0;
Matches 26; Conservative 0; Db 74 VWE PASHEGGEREV ASQHTKOPSHS 99

RESULT 2
F771326 hypothetical protein TP0433 - syphilis spirochete
C.Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C.Date: 24-Jul-1998 #Sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C.Accession: F771326
R.Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwilymson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McElroy, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A.Title: Complete genome sequence of *Treponema pallidum*, the syphilis spirochete.
A.Reference number: A71250; MUID:98332770; PMID:9665876
A.Accession: F771326
A.Status: preliminary; nucleic acid sequence not shown; translation not shown
A.Molecule type: DNA
A.Residues: 1-256 <CDS>
A.Cross-references: UNIPROT:OB3448; GB:AB001220; GB:AE000520; NID:93322705; PIDN: AAC654
A.Experimental source: strain Nichols
A.Genetics: C;Genetics:
A.Gene: Tp0433
Query Match 45.3%; Score 62; DB 2; Length 256;

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OM protein - protein search, using sw model

Run on: January 28, 2005, 10:59:24 ; Search time 24.6359 Seconds

378.592 Million cell updates/sec

Title: US-10-017-168-14

Perfect score: 137

Sequence: 1 VVEPASGEGGEREVASQHTKOPSHS 26

Scoring table: BLOSUM62

Gapov 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_21sep04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003s:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description	RESULT	ALIGNMENTS
1	137	100.0	26	AAB48326	AAB48326	
2	137	100.0	432	AAB48316	AAB48326;	
3	121	88.3	232	AAB48317	XX	
4	121	88.3	312	AAB48318	DT	20-APR-2001 (first entry)
5	69	50.4	20	AAB48330	XX	T. pallidum acidic repeat protein immunogenic peptide arp 8.
6	62	45.3	20	AAB48321	XX	Treponema pallidum; acidic repeat protein; arp; immunogenic; syphilis; yaws; bejel.
7	62	45.3	21	AAB48325	XX	Treponema pallidum.
8	56	40.9	339	AAB18291	XX	OS
9	53	38.7	20	AAB48328	XX	PN
10	53	38.7	20	AAB48328	XX	W020077486-A2.
11	53	38.7	20	AAB48327	XX	PD
12	53	38.7	683	AAB4887	XX	21-DEC-2000.
13	52	38.0	349	AAB077085	XX	PP
14	52	38.0	478	AAB192051	XX	14-JUN-1999; 99US-0138981P.
15	51.5	37.6	330	AAB94271	PA	(USSH) US DEPT HEALTH & HUMAN SERVICES.
16	51.5	37.6	330	AAB94001	XX	Liu H, Steiner B, Rhodes B;
17	51.5	37.6	330	ADJ170056	PI	WPI; 2001-080711/09.
18	51.5	37.6	572	AAB14734	DR	PT Detecting Treponema pallidum in blood, saliva, etc., by detecting formation of a complex between immunogenic peptides of acidic repeat protein of the bacterium and an antibody present in the biological sample.
19	51	37.2	70	AAB14734	XX	PT Detecting Treponema pallidum in blood, saliva, etc., by detecting formation of a complex between immunogenic peptides of acidic repeat protein of the bacterium and an antibody present in the biological sample.
20	51	37.2	70	AAB33699	XX	PT Detecting Treponema pallidum in blood, saliva, etc., by detecting formation of a complex between immunogenic peptides of acidic repeat protein of the bacterium and an antibody present in the biological sample.
21	51	37.2	70	AAM27157	XX	PT Detecting Treponema pallidum in blood, saliva, etc., by detecting formation of a complex between immunogenic peptides of acidic repeat protein of the bacterium and an antibody present in the biological sample.
22	51	37.2	70	AAB28514	XX	PT Detecting Treponema pallidum in blood, saliva, etc., by detecting formation of a complex between immunogenic peptides of acidic repeat protein of the bacterium and an antibody present in the biological sample.
23	51	37.2	70	AAB19148	XX	PT Detecting Treponema pallidum in blood, saliva, etc., by detecting formation of a complex between immunogenic peptides of acidic repeat protein of the bacterium and an antibody present in the biological sample.
24	51	37.2	70	AAM66872	XX	PT Detecting Treponema pallidum in blood, saliva, etc., by detecting formation of a complex between immunogenic peptides of acidic repeat protein of the bacterium and an antibody present in the biological sample.
25	51	37.2	70	AAM54467	XX	PT Detecting Treponema pallidum in blood, saliva, etc., by detecting formation of a complex between immunogenic peptides of acidic repeat protein of the bacterium and an antibody present in the biological sample.

ABG48537 Human liv
AAM02456 Peptide #
ABG36529 Human pep
ABG70847 Pseudopep
ABG8621 Drosophil
ABG68024 Drosophil
ABG83532 Breast sp
ABG83529 Breast sp
ABG13074 Novel hum
ABG13075 Novel hum
ABG09109 Novel pro
ABG42456 Human ova
ABG8527 Breast sp
ABG83530 Breast sp
ABG75357 Pseudomon
Aau96770 Lycopersici
ABG13745 Pseudomon
Aab15090 Human ner
Aau45385 Propionib
Abo1904 Propionib

ABG48537 Human liv
AAM02456 Peptide #
ABG36529 Human pep
ABG70847 Pseudopep
ABG8621 Drosophil
ABG68024 Drosophil
ABG83532 Breast sp
ABG83529 Breast sp
ABG13074 Novel hum
ABG13075 Novel hum
ABG09109 Novel pro
ABG42456 Human ova
ABG8527 Breast sp
ABG83530 Breast sp
ABG75357 Pseudomon
Aau96770 Lycopersici
ABG13745 Pseudomon
Aab15090 Human ner
Aau45385 Propionib
Abo1904 Propionib

ABG48537 Human liv
AAM02456 Peptide #
ABG36529 Human pep
ABG70847 Pseudopep
ABG8621 Drosophil
ABG68024 Drosophil
ABG83532 Breast sp
ABG83529 Breast sp
ABG13074 Novel hum
ABG13075 Novel hum
ABG09109 Novel pro
ABG42456 Human ova
ABG8527 Breast sp
ABG83530 Breast sp
ABG75357 Pseudomon
Aau96770 Lycopersici
ABG13745 Pseudomon
Aab15090 Human ner
Aau45385 Propionib
Abo1904 Propionib

ABG48537 Human liv
AAM02456 Peptide #
ABG36529 Human pep
ABG70847 Pseudopep
ABG8621 Drosophil
ABG68024 Drosophil
ABG83532 Breast sp
ABG83529 Breast sp
ABG13074 Novel hum
ABG13075 Novel hum
ABG09109 Novel pro
ABG42456 Human ova
ABG8527 Breast sp
ABG83530 Breast sp
ABG75357 Pseudomon
Aau96770 Lycopersici
ABG13745 Pseudomon
Aab15090 Human ner
Aau45385 Propionib
Abo1904 Propionib

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OM protein - protein search, using bw model

Run on: January 28, 2005, 10:59:24 ; Search time 18.9507 Seconds
(without alignments)
Scoring table: BLOSUM62

Title: US-10-017-168-15

Perfect score: 101
Sequence: 1 EVEDVVKVNEPASEREGGER 20

Searched: Gapext 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Database : Listing first 45 summaries
A_Geneseq_21Sep04: *
1: geneseqp1980s: *
2: geneseqp1990s: *
3: geneseqp2000s: *
4: geneseqp001s: *
5: geneseqp2002s: *
6: geneseqp2003ab: *
7: geneseqp2003bs: *
8: geneseqp2004bs: *

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description
1 101 100.0 20 4 AAB48327 Ab43327 T. pallidum
2 100 100.0 232 4 AAB4317 Ab43317 T. pallidum
3 101 100.0 312 4 AAB48318 Ab43318 T. pallidum
4 101 100.0 432 4 AAB48316 Ab43316 T. pallidum
5 97 96.0 20 4 AAB48329 Ab43329 T. pallidum
6 96 95.0 20 4 AAB48328 Ab43320 T. pallidum
7 87 86.1 20 4 AAB48320 Ab43320 T. pallidum
8 82 81.2 20 4 AAB48330 Ab43330 T. pallidum
9 77 76.2 20 4 AAB48325 Ab43325 T. pallidum
10 65 64.4 21 4 AAB48325 Ab43325 T. pallidum
11 60 59.4 19 4 AAB48319 Ab43319 T. pallidum
12 53 52.5 26 4 AAB48326 Ab43326 T. pallidum
13 50 49.5 79 3 AAG61691 Arabidopsis
14 50 49.5 187 3 AAG16629 Arabidopsis
15 50 49.5 187 3 AAG50350 Arabidopsis
16 49 48.5 170 6 AD55215 Human pro
17 49 48.5 266 4 AAB80279 Ab80279 Human pro
18 49 48.5 266 4 AAB64379 Human pro
19 48.5 266 4 AAM39738 Human pol
20 49 48.5 277 4 AAB80305 Human pro
21 49 48.5 277 4 AAB80347 Human pro
22 49 48.5 288 4 AAB80343 Human pro
23 49 48.5 289 4 AAM41524 Human pol
24 49 48.5 304 3 AAB57037 Human pro
25 49 48.5 519 6 ABU20235 Protein e

26 48 47.5 296 4 ABG315624 Novel hum
27 48 47.5 547 6 ABM1567
28 48 47.5 754 7 AD336201 Klebsiell
29 48 47.5 754 7 AD336160 Klebsiell
30 47.5 47.0 792 4 AAG82199 Hag82199 S. epider
31 47.5 47.0 801 5 ABB40739 Abp40739 Staphyloc
32 47 46.5 117 6 AD15777 Hag15777 Human GAG
33 47 46.5 117 7 ADB65417 Hag65417 Human GAG
34 47 46.5 510 8 ADQ08680 Hag08680 Clona int
35 47 46.5 1022 4 ABG02687 Hag02687 Novel hum
36 47 46.5 1278 6 ABG74682 Abg74682 Human CGD
37 47 46.5 2091 8 ADN61449 Abn61449 Human pro
38 47 46.5 2193 6 ABB42219 Human pro
39 47 46.5 2219 8 ADN00364 Adn00364 Novel hum
40 47 46.5 2245 8 ADN96651 Adn96651 Human Nim
41 46 46.5 571 7 AB077402 Pseudomon
42 46 45.5 60 5 ABB34774 Abp34774 Human ORF
43 46 45.5 171 3 AAG8178 Abg8178 Arabidops
44 46 45.5 197 3 AAG08177 Abg08177 Arabidops
45 46 45.5 226 3 AAG08176 Abg08176 Arabidops

ALIGNMENTS
RESULT 1
ID AAB48327
XX
XX
AC AAB48327;
XX
XX
DT 20-APR-2001 (first entry)
XX
DE T. pallidum acidic repeat protein immunogenic peptide arp 9.
XX
KW Treponema pallidum; acidic repeat protein; arp; immunogenic; syphilis;
KW yawa; bejel.
XX
OS Treponema pallidum.
XX
PN WO20077486-X2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 99US-0138981P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Liu H, Steiner B, Rhodes B;
XX
DR WPI; 2001-080711/09.
XX
PT Detecting Treponema pallidum in blood, saliva, etc., by detecting
formation of a complex between immunogenic peptides of acidic repeat
protein of the bacterium and an antibody present in the biological
sample.
PT
PT
PT
XX
PS Claim 15; Fig 11; 73pp; English.

CC
The invention relates to a method of detecting presence of Treponema pallidum (TP), anti-treponemal antibodies (Ab), or both in a biological sample that involves contacting an acidic repeat protein (arp), or one or more isolated immunogenic TP peptides of arp with an Ab containing an Ab containing a biological sample and then detecting the formation of a complex between immunogenic peptides and Ab. The presence of the complex indicates the presence of TP. The method is thus useful for diagnosing syphilis, yaws, and bejel diseases. The immunogenic Peptides or the Ab raised against arp, as part of an immunogenic composition, are useful for inducing a protective immune response against syphilis, yaws or bejel caused by TP. Sequences AAB48319-AB48330 represent immunogenic peptides of T. pallidum arp protein

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OM protein - protein search, using sw model

Run on: January 28, 2005, 11:05:24 ; Search time 3.11606 Seconds
(without alignments)

617.555 Million cell updates/sec

Title: US-10-017-168-15

Perfect score: 101 ; Sequence: 1 EVEDVPKVVEPASEREGGER 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0 ; Maximum DB seq length: 200000000

Post-processing: Maximum Match 0% ; Listing first 45 summaries

Database : PIR_79;*

1: pir1;*
2: pir2;*
3: pir3;*
4: pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID

Description

Query	Match	96 0%	Score	97	DB	2	Length	256
Best Local Similarity	95.0%		Pred. No.	3.8e-07		1	Indels	0
Matches	19		Mismatches	0			Gaps	0
Conservative								

Db 184 EVEDVPKVVEPASEREGGER 203

RESULT 2

Query	Match	96 0%	Score	97	DB	2	Length	256
Best Local Similarity	95.0%		Pred. No.	3.8e-07		1	Indels	0
Matches	19		Mismatches	0			Gaps	0
Conservative								

Db 184 EVEDVPKVVEPASEREGGER 203

ALIGNMENTS

RESULT 1

F71326

hypothetical protein TP033 - syphilis spirochete

C;Species: *Treponema pallidum* subsp. *pallidum* (syphilis spirochete)

C;Accession: F71326 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004

R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwinn, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDowell, L.; Weidman, J.; Smith, H.O.; Venter, J.C.

Science 281, 375-388, 1998

A;Title: Complete genome sequence of *Treponema pallidum*, the syphilis spirochete.

A;Reference number: A71250; MUID:98332770; PMID:9665876

A;Accession: F71326

A;Status: Preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-256 <COL>

A;Cross-references: UNIPROT:083448; GB:AE001220; GB:AB000520; NID:93322705; PIDN: AAC654

A;Experimental source: strain Nichols

C;Genetics: A;Gene: TP0433

Query Match 96 0% ; Score 97 ; DB 2 ; Length 256;

Best Local Similarity 95.0% ; Pred. No. 3.8e-07 ; Indels 0 ; Gaps 0 ;

Matches 19 ; Conservative 0 ; Mismatches 0 ;

Db 184 EVEDVPKVVEPASEREGGER 203

Query Match 96 0% ; Score 97 ; DB 2 ; Length 256;

Best Local Similarity 95.0% ; Pred. No. 3.8e-07 ; Indels 0 ; Gaps 0 ;

Matches 19 ; Conservative 0 ; Mismatches 0 ;

Db 184 EVEDVPKVVEPASEREGGER 203

hypothetical protein TP0434 - syphilis spirochete

C;Species: *Treponema pallidum* subsp. *pallidum* (syphilis spirochete)

C;Accession: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004

R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwinn, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDowell, L.; Weidman, J.; Smith, H.O.; Venter, J.C.

Science 281, 375-388, 1998

A;Title: Complete genome sequence of *Treponema pallidum*, the syphilis spirochete.

A;Reference number: A71250; MUID:98332770; PMID:9665876

A;Accession: F71326

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-227 <COL>

A;Cross-references: UNIPROT:083449; GB:AE001220; GB:AB000520; NID:93322705; PIDN: AAC654

A;Experimental source: strain Nichols

C;Genetics: A;Gene: TP0434

Query Match 81.2% ; Score 82 ; DB 2 ; Length 227 ;

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OM protein - protein search, using sw model

Run on: January 28, 2005, 11:12:20 ; Search time 17.5517 Seconds.

Sequence: (without alignments) 655.635 Million cell updates/sec

Title: US-10-017-168-15
perfect score: 101
Sequence: 1 EVEDVPKVVEPASEREGGER 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 02;*

1: uniprot_sprot;*

2: uniprot_trembl;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	101	100.0	348	2 Q9ALV7
2	101	100.0	393	2 Q93CA3
3	101	100.0	428	2 Q9ALV6
4	101	100.0	432	2 Q51953
5	101	100.0	548	2 Q93CA4
6	97	96.0	256	2 Q33448
7	82	81.2	227	2 Q83449
8	51.5	51.0	153	1 Y862-METH
9	50	49.5	187	2 Q851J8
10	50	49.5	193	2 Q941I5
11	50	49.5	238	2 Q6RRP9
12	50	49.5	1174	2 Q82Q43
13	49	49.5	1174	2 BAC98029
14	49	48.5	256	2 Q8WV22
15	48	47.5	482	2 Q6xQ57
16	48	47.5	482	2 AK037694
17	48	47.5	547	2 P5090
18	48	47.5	547	2 Q7TXB8
19	48	47.5	2192	2 Q81BW7
20	47.5	47.0	792	2 Q8CPY0
21	47	46.5	178	2 CAG14983
22	47	46.5	266	2 Q97J20
23	47	46.5	267	2 Q8K2B4
24	47	46.5	280	2 Q8K2B4
25	47	46.5	280	2 Q9CY20
26	47	46.5	308	2 Q89494
27	47	46.5	357	2 Q62AB0
28	47	46.5	357	2 BAD03360
29	47	46.5	1159	2 Q91NM8
30	47	46.5	1165	2 Q7JKP6
31	47	46.5	1165	2 CAP31485

RESULT 1	ID	PRELIMINARY;	PRT;	348 AA.
Q9ALV7	Q9ALV7	Q9ALV7;	DT	01-JUN-2001 (TREMBLrel. 17, Created)
			DT	01-DEC-2001 (TREMBLrel. 19, Last Sequence update)
			DT	01-OCT-2002 (TREMBLrel. 22, Last annotation update)
			DE	Acidic repeat protein.
			GN	Name=arp;
			OS	Treponema pallidum (subsp. pertenue) (Yaws treponeme).
			OC	Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
			OX	NCBI_TaxID=168;
			RN	[1]
			RP	SEQUENCE FROM N.A.
			RA	STRAIN=CD2;
			RA	Liu H., Steiner B.;
			RA	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
			RN	[2]
			RP	SEQUENCE FROM N.A.
			RC	STRAIN=CD2;
			RL	Liu H., Steiner B.M., Rodes B.;
			RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
			DR	EMBL: AF442806; AX01460.2; -.
			SQ	SEQUENCE 348 AA; 37936 MW; E4A446BD82344592 CRC64;
			Query	Match 100.0%; Score 101; DB 2; Length 348;
			Best	Local Similarity 100.0%; Pred. No 6.2e-07;
			Matches	Conservative 0; NMatches 0; Indels 0; Gaps 0;
			Qy	1 EVEDVPKVVEPASEREGGER 20
			Db	128 EVEDVPKVVEPASEREGGER 147

RESULT 2	ID	PRELIMINARY;	PRT;	393 AA.
Q93CA3	Q93CA3	Q93CA3;	DT	01-DEC-2001 (TREMBLrel. 19, Created)
			DT	01-DEC-2001 (TREMBLrel. 19, Last Sequence update)
			DT	01-OCT-2002 (TREMBLrel. 22, Last annotation update)
			DE	Acidic repeat protein.
			GN	Name=arp;
			OS	Treponema pallidum (subsp. pertenue) (Yaws treponeme).
			OC	Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
			OX	NCBI_TaxID=168;
			RN	[1]
			RP	SEQUENCE FROM N.A.
			RC	STRAIN=CD2;
			RA	Liu H., Steiner B.M., Rodes B.;
			RA	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
			DR	EMBL: AF411126; AAL07373.1; -.
			SQ	SEQUENCE 393 AA; 42852 MW; C2D9198AA1BB82B5 CRC64;

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OM protein - protein search, using sw model

Run on: January 28, 2005, 10:59:24 ; Search time 18.9507 Seconds
 (without alignments)
 378.592 Million cell updates/sec

Title: US-10-017-168-16

Perfect score: 101

Sequence: 1 EENVPKVNEPASEREGGER 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 0

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_21Sep04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003abs:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT 1
 AAB48328
 ID AAB48328 standard; peptide; 20 AA.
 XX
 AC AAB48328;
 XX
 DT 20-APR-2001 (first entry)
 XX
 DE T. pallidum acidic repeat protein immunogenic peptide arp 10.
 XX
 KW Treponema pallidum; acidic repeat protein; arp; immunogenic; syphilis;
 KW yaws; bejel.
 XX
 OS Treponema pallidum.
 XX
 PN WO200077486-A2.
 XX
 FD 21-DBCC-2000.
 XX
 FF 14-JUN-2000; 2000MO-US016425.
 XX
 PR 14-JUN-1999; 99US-0139981P.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Liu H, Steiner B, Rhodes B;
 XX
 DR WPI; 2001-080711/09.
 XX
 PT Detecting Treponema pallidum in blood, saliva, etc., by detecting formation of a complex between immunogenic peptides of acidic repeat protein of the bacterium and an antibody present in the biological sample.
 XX
 CL Claim 15; Fig 11; 73pp; English.

The invention relates to a method of detecting presence of Treponema pallidum (TP), anti-treponemal antibodies (Abs), or both in a biological sample that involves contacting an acidic repeat protein (arp), or one or more isolated immunogenic TP peptides of arp with an Ab containing biological sample and then detecting the formation of a complex between immunogenic peptides and Ab. The presence of the complex indicates the presence of TP. The method is thus useful for diagnosing syphilis, yaws, and bejel diseases. The immunogenic peptides or the Abs raised against arp, as part of an immunogenic composition, are useful for inducing a protective immune response against syphilis, yaws or bejel caused by TP.

Sequences AAB48319-AAB48330 represent immunogenic peptides of T. pallidum arp protein. AAB48319-AAB48330 represent immunogenic peptides of T. pallidum arp protein.

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OM protein - protein search, using sw model.

Run on: January 28, 2005, 11:05:24 ; Search time 3.11606 Seconds

(without alignments) 617.555 Million cell updates/sec

Title: US-10-017-168-16
Perfect score: 101
Sequence: 1 EVENVPKVVEPASEREGGER 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR 79;*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. 18 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Length DB ID

Description

1 92 91.1 256 2 P71326 hypothetical protein Tp0433 - syphilis spirochete
2 78 77.2 227 2 G71326 hypothetical prote
3 50 49.5 184 2 D84603 hypothetical prote
4 47 46.5 308 2 T11946 hypothetical prote
5 46.5 46.0 153 1 B62215 conserved hypothetical
6 46 45.5 897 2 E9202 valine-tRNA ligase
7 46 45.5 1350 2 G36793 hypothetical prote
8 45 44.6 220 2 S24685 CAMP response elem
9 45 44.6 344 2 JC5602 CAMP response elem
10 45 44.6 684 1 S22700 hypothetical protein Tp0434 - syphilis spirochete
11 44 43.6 178 2 E99994 amphiphysin - chick
12 44 43.6 217 2 C37944 hypothetical prote
13 44 43.6 229 2 B37944 CAMP response elem
14 44 43.6 229 2 A77944 CAMP response elem
15 44 43.6 278 2 S3101 CAMP response elem
16 44 43.6 312 2 E64072 CAMP response elem
17 44 43.6 341 2 S20827 spermidine/putresc
18 44 43.6 341 2 S26668 CAMP response elem
19 44 43.6 793 2 S67070 GAC1 protein - yeast
20 44 43.6 99 2 A55819 nonhistone chromos
21 43 42.6 229 2 S56687 histone H2B153 - w
22 43 42.6 135 2 F71326 hypothetical prote
23 43 42.6 289 2 T01257 probable GTP-1-like
24 43 42.6 313 2 D86668 oligopeptide ABC t
25 42.6 315 2 D81131 hypothetical prote
26 43 42.6 356 2 B71023 hypothetical prote
27 43 42.6 382 2 T0301 hypothetical prote
28 43 42.6 547 2 E70650 phosphoglucomutase

ALIGNMENTS

Result No. Score Query Length DB ID

Description

RESULT 1
F71326 hypothetical protein Tp0433 - syphilis spirochete
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C;Accession: P71326
R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gw
ison, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; Mc
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
A;Title: Complete Genome Sequence of Treponema pallidum, the syphilis spirochete.
A;Reference number: A71250; NID:98332770; PMID:9655976
A;Accession: P7136
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-256 <COL>
A;Cross-references: UNIPROT:083449; GB:AE001220; GB:AE000520; NID:93322705; PIDN: AAC65
A;Experimental source: strain Nichols
A;Gene: Tp0433
A;Gene: Tp0433

Query Match 91.1%; Score 92; DB 2; Length 256;
Best Local Similarity 90.0%; Pred. No. 1.6e-06; 1; Mismatches 0; Gaps 0;
Matches 18; Conservative 1; Indels 0; Gaps 0;
Oy 1 EVENVPKVVEPASEREGGER 20
Db 184 EVENVPKVVEPASEREGGER 203

RESULT 2
G71326 hypothetical protein Tp0434 - syphilis spirochete
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C;Accession: G71326
R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gw
ison, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; Mc
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A;Reference number: A71250; NID:98332770; PMID:9655976
A;Accession: G71326
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-227 <COL>
A;Cross-references: UNIPROT:083449; GB:AE001220; GB:AE000520; NID:93322705; PIDN: AAC65
A;Experimental source: strain Nichols
A;Gene: Tp0434

Query Match 77.2%; Score 78; DB 2; Length 227;

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OM protein - protein search, using sw model

Run on: January 28, 2005, 10:59:24 ; Search time 18.9507 Seconds
(without alignments) 378.592 Million cell updates/sec

Title: US-10-017-168-17
Perfect score: 101

Sequence: 1 EYEDAPKVVEPASEREGGER 20

Scoring table: BLOSUM62
GapOp 10.0 , Gapext 0.5

Searched: 200273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 200273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21Sep04:
1: geneseqp1980s: *
2: geneseqp1990s: *
3: geneseqp2000s: *
4: geneseqp2001s: *
5: geneseqp2002s: *
6: geneseqp2003as: *
7: geneseqp2003bs: *
8: geneseqp2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	101	100.0	20	AAB48329
2	101	100.0	432	AAB48316
3	97	96.0	20	Aab49327
4	97	96.0	232	Aab48317
5	97	96.0	312	Aab48318
6	92	91.1	20	AAB48328
7	91	90.1	40	AAB48320
8	78	77.2	20	AAB48330
9	77	76.2	4	AAB48321
10	65	64.4	21	AAB48325
11	64	63.4	19	AAB48319
12	53	52.5	26	AAB48326
13	48	47.5	296	4 ABB15624
14	47	46.5	79	3 AAG61591
15	47	45.5	187	3 AAG16629
16	47	45.5	187	3 AAG50350
17	47	46.5	434	3 AAG38717
18	47	46.5	3	AAG08216
19	47	46.5	434	5 ABB92639
20	47	46.5	612	4 ABB7174
21	47	46.5	763	3 AAY32375
22	46	45.5	261	8 ADJ76332
23	46	45.5	437	4 AAB50661
24	46	45.5	547	6 ABBM15867
25	46	45.5	571	7 ABB077402

Maximum DB seq length: 0

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21Sep04:
1: geneseqp1980s: *
2: geneseqp1990s: *
3: geneseqp2000s: *
4: geneseqp2001s: *
5: geneseqp2002s: *
6: geneseqp2003as: *
7: geneseqp2003bs: *
8: geneseqp2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

26	46	45.5	1007	4 AAB50660	C. elegan
27	46	45.5	1226	3 AAG52239	Aag52239 Arabidops
28	46	45.5	1321	3 AAG42238	Aag42238 Arabidops
29	46	45.5	1351	3 AAG42237	Aag42237 Arabidops
30	45	44.6	109	4 AAU0366	Aau0366 Propionib
31	45	44.6	109	6 ABBM6985	Abm2685 Propionib
32	45	44.6	170	6 ADA55215	Ada55215 Human pro
33	45	44.6	266	4 AAB80279	Aab80279 Human pro
34	45	44.6	265	4 AAB64379	Aab64379 Amino aci
35	45	44.6	266	4 AAM37738	Aam9738 Human pol
36	45	44.6	277	4 AAB0305	Aab80305 Human pro
37	45	44.6	277	4 AAB80347	Aab80347 Human pro
38	45	44.6	288	4 AAB80343	Aab80343 Human pro
39	45	44.6	289	4 AAM41524	Aam41524 Human pol
40	45	44.6	304	3 AAB57037	Aab5737 Human pro
41	45	44.6	510	8 ADQ8686	Adq8680 Ciona int
42	45	44.6	519	6 ABU20235	Abu20235 Protein e
43	45	44.6	579	8 AAC04552	Aac04552 Murine BH
44	45	44.6	944	4 ABB60979	Ab60979 Drosophili
45	44.6	1841	2 AAW22605	Aaw22605 Tyiactone	

The invention relates to a method of detecting presence of *Treponema pallidum* (Tp), anti-treponemal antibodies (Abs), or both in a biological sample that involves contacting an acidic repeat protein (arp) or one or more isolated immunogenic Tp peptides or arp with an Ab containing biological sample and then detecting the formation of a complex between immunogenic peptides and Ab. The presence of the complex indicates the presence of Tp. The method is thus useful for diagnosing syphilis, yaws, and bejel diseases. The immunogenic peptides or the Abs raised against arp, as part of an immunoconjugate, are useful for inducing a protective immune response against syphilis, yaws or bejel caused by Tp. Sequences AAB48319-AAB48330 represent immunogenic peptides of *T. pallidum* arp protein.

Copyright (c) 1993 - 2005 Compugen Ltd.	Gencore Version 5.1.6											
OM protein - protein search, using sw model												
Run on:	January 28, 2005, 11:12:20 ; Search time 17.5517 Seconds											
Title:	US-10-017-168-17											
Perfect score:	101 (without alignment) 655,633 Million cell updates/sec											
Sequence:	1 EVERDAKPKVVERPASEREGGER 20											
Scoring table:	BLOSUM42											
Gapop 10.0 , Gapext 0.5												
Searched:	1825181 seqs, 575374646 residues											
Total number of hits satisfying chosen parameters:	1825181											
Minimum DB seq length: 0												
Maximum DB seq length: 2000000000												
Post-processing:	Minimum Match 0% Maximum Match 100% Listing First 45 summaries											
Result												
No.	Score	Query	Match	Length	DB	ID	Description					
1	101	100.0	256	2	083448	083448	PRELIMINARY; AC: 083448;	PRT:	256 AA.			
2	101	100.0	432	2	051953	051953	DT: 01-NOV-1998 (TREMBLrel. 08, Created)					
3	101	100.0	548	2	093484	093484	DT: 01-NOV-1998 (TREMBLrel. 08, Last Sequence update)					
4	97	96.0	348	2	094ALV7	094ALV7	DT: 01-JUN-2003 (TREMBLrel. 24, Last annotation update)					
5	97	96.0	393	2	093CA3	093CA3	DE: Hypothetical protein TP0433.					
6	97	96.0	428	2	094LIV6	094LIV6	OS: Treponema pallidum.					
7	78	77.2	227	2	083449	083449	OC: Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.					
8	52	51.5	2192	2	081Bw7	081Bw7	NCBI_TaxID=160;					
9	51	50.5	1165	2	07JKP6	07JKP6	[1] SEQUENCE FROM N.A.					
10	51	50.5	1165	2	CAT31485	CAT31485	RA: STRAIN=Nichols;					
11	50	49.5	434	2	Q7STU6	Q7STU6	RX: MEDLINE=98332770; PubMed=9663876;					
12	50	49.5	434	2	093X74	093X74	RA: Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,					
13	50	49.5	434	2	BAD14934	BAD14934	RA: Dodson R.J., Gwinn M.L., Hickley E.K., Clayton R.A., Ketchum K.A.,					
14	50	49.5	572	1	SYR CHRVO	SYR CHRVO	RA: Sodergren E., Hardham J.M., McLeod M.P., Salzberg S.L., Peterson J.D.,					
15	49	48.5	151	2	084BS1	084BS1	RA: Khalak H.G., Richardson D.L., Howell J.K., Chidambaram M., Utterback R., McDonald L.A., Attieach P., Bowman C., Coton M.D.,					
16	49	48.5	294	2	06UGG2	06UGG2	RA: Fujii C., Garland S.A., Hatch B., Horst K.M., Sandusky M.,					
17	49	48.5	294	2	AAR90407	AAR90407	RA: Weidman J.P., Smith H.O., Venter J.C.;					
18	47.5	47.5	769	2	Q75BK7	Q75BK7	RT: "Complete genome sequence of Treponema pallidum, the syphilis					
19	48	47.5	769	2	AKB51490	AKB51490	RT: Spirochete.;					
20	48	47.5	2223	2	Q81D12	Q81D12	RL: Science 281:375-388 (1998);					
21	47	47.5	153	1	Y862-METH	Y862-METH	DR: AEG01220; AAC654211; -					
22	47	46.5	130	2	08CC10	08CC10	DR: PIR; F71326; F71326.					
23	47	46.5	168	2	Q81H12	Q81H12	DR: TPI033; -					
24	47	46.5	187	2	Q81J8	Q81J8	DR: 01-JUN-1998 (TREMBLrel. 06, Created)					
25	47	46.5	193	2	Q94115	Q94115	DT: 01-JUN-1998 (TREMBLrel. 06, Last Sequence update)					
26	47	46.5	210	2	Q94A20	Q94A20	DT: 01-OCT-2002 (TREMBLrel. 22, Last annotation update)					
27	47	46.5	344	2	Q89hg0	Q89hg0	DE: Acidic repeat protein.					
28	47	46.5	357	2	Q62AE0	Q62AE0	OS: Treponema pallidum.					
29	47	46.5	357	2	BAD03360	BAD03360	OC: Bacteria; Spirochaetes; Spirochaetales; Treponema.					
30	47	46.5	434	1	MDP3-ARATH	MDP3-ARATH	OX: NCBI_TaxID=160;					
31	47	46.5	612	1	Q9vg45	Q9vg45	[1] SEQUENCE FROM N.A.					

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 28, 2005, 10:59:24 ; Search time 18.9507 Seconds
(without alignments)
3.78.592 Million cell updates/sec

Title: US-10-017-168-18
Perfect score: 106
Sequence: 1 EVEDVPGVVERPASCHEGGER 20

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	106	100.0	20	AAB48330
2	106	100.0	4	AAB48316
3	82	77.4	20	AAB48327
4	82	77.4	232	AAB48317
5	82	77.4	312	AAB48318
6	78	73.5	20	AAB48329
7	77	72.6	20	AAB48328
8	69	65.1	26	AAB48326
9	68	64.2	20	AAB48320
10	58	54.7	20	AAB48321
11	55	51.9	754	7 ADD36201
12	55	51.9	754	7 ADD36201
13	53	50.0	19	AAB48319
14	53	50.0	21	AAB48325
15	52	49.1	211	4 AAB67561
16	52	49.1	211	6 ABB64080
17	52	49.1	307	6 ABB6113
18	52	49.1	754	7 ADD36210
19	52	49.1	754	7 ADD36219
20	52	49.1	754	7 ADD36207
21	52	49.1	754	7 ADD36198
22	52	49.1	754	7 ADD36222
23	52	49.1	754	7 ADD36228
24	52	49.1	754	7 ADD36163
25	52	49.1	754	7 ADD36204

ALIGNMENTS

26	52	49.1	754	7 ADB36234	Ade36234 Klebsiell
27	52	49.1	754	7 ADB36216	Ade36216 Klebsiell
28	52	49.1	754	7 ADB36249	Ade36249 Klebsiell
29	52	49.1	754	7 ADB36213	Ade36213 Klebsiell
30	52	49.1	754	7 ADB36237	Ade36237 Klebsiell
31	52	49.1	754	7 ADB36225	Ade36225 Klebsiell
32	52	49.1	754	7 ADB36240	Ade36240 Klebsiell
33	52	49.1	754	7 ADB36246	Ade36246 Klebsiell
34	52	49.1	754	7 ADB36231	Ade36231 Klebsiell
35	52	49.1	754	7 ADB36243	Ade36243 Klebsiell
36	51.5	48.6	228	7 ABB084152	Abo84152 Pseudomon
37	50.5	47.6	76	4 AABU60228	Aiu60228 Propionib
38	50.5	47.6	76	6 ABBM56747	Alm56747 Propionib
39	50	47.2	340	8 ADB46982	Adn46982 Thermococ
40	50	47.2	350	6 ABBU6303	Ahu6303 Protein e
41	50	47.2	394	7 ABBOT9086	Abo79086 Pseudomon
42	50	47.2	1504	7 ABBOT77862	Ad44887 Rat Prote
43	49.5	46.7	683	7 ABB44887	Ad44887 Rat Prote
44	49	46.2	1938	6 ABB76679	Ahp76679 Streptomy
45	48.5	45.8	2044	4 ABB61488	Ahh61488 Drosophi

The invention relates to a method of detecting presence of *Treponema pallidum* (TP), anti-treponemal antibodies (Abs), or both, in a biological sample that involves contacting an acidic repeat protein (arp), or one or more isolated immunogenic TP peptides of arp with an Ab containing immunogenic peptides and Ab. The presence of the complex indicates the presence of TP. The method is thus useful for diagnosing Syphilis, yaws, and bejel diseases. The immunogenic peptides or the Abs raised against arp, as part of an immunogenic composition, are useful for inducing a protective immune response against syphilis, yaws or bejel caused by TP. Sequences AAB48319-AAB48330 represent immunogenic peptides of *T. pallidum* arp protein.

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OM protein - protein search, using SW model

Run on: January 28, 2005, 11:12:20 ; Search time 17.5517 Seconds
(without alignments)

Title: US-10-017-168-18
Perfect score: 106
Sequence: 1 EVEDVPGVVEPASGHGEGGER 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqB, 575374646 residues

Total number of hits satisfying chosen parameters:
Minimum DB seq length: 0

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 02-*
1: uniprot_sprot;*

2: uniprot_trembl;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match length DB ID Description

1 100.0 227 2 083449

083449 treponema p

051953 treponema p

093ca4 treponema p

09alv7 treponema p

093ca3 treponema p

09alv6 treponema p

083448 treponema p

07u893 synechococc

08x2j ralstonia s

075b14 ashyba goss

093ca3 ashyba goss

09alv6 treponema p

083448 treponema p

07u893 synechococc

08x2j ralstonia s

075b14 ashyba goss

093ca3 ashyba goss

09alv6 treponema p

083448 treponema p

07u893 synechococc

08x2j ralstonia s

075b14 ashyba goss

093ca3 ashyba goss

09alv6 treponema p

083448 treponema p

07u893 synechococc

RESULT 1		PRELIMINARY:		PRT:	227 AA.
ID	083449	AC	083449;	DT	01-NOV-1998 (TREMBLrel. 08, Created)
				DT	01-NOV-1998 (TREMBLrel. 08, Last sequence update)
				DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DB				DB	Hypothetical protein TP0434.
GN				GN	Orderredicustisomes=TP0434;
OS				OS	Treponema pallidum.
OC				OC	Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
RN				RN	NCBI_TaxID=160;
RP				RP	SEQUENCE FROM N.A.
RC				RC	STRAIN=Nichols;
RX				RX	Medline:9833270; PubMed=9665876;
RA				RA	Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.C.,
RA				RA	Dodson R.J., Gwinn M.L., Hickey E.K., Clayton R.A., Ketchum K.A.,
RA				RA	Sodergren E., Hardham J.M., McLeod M.P., Salzberg S.L., Peterson J.D.,
RA				RA	Khalak H.G., Richardson D.L., Howell J.M., Chidambaram M., Utterback T.R., McDonald L.A., Artichak P., Bowman C., Cottam M.D., Fujii C., Garland S.A., Hatch B., Horst K., Roberts K.M., Sandusky M.,
RA				RA	Weldman J.H., Smith H.C., Venter J.C.;
RT				RT	"Complete genome sequence of Treponema pallidum, the syphilis spirochete."
RL				RL	Science 281:375-388 (1998);
EMBL				EMBL	AB001220; AAC65422.1; -.
DR				DR	PIR; G71326; G71326.
DR				DR	TIGR; TP0434; -.
DR				DR	Complete proteome: Hypothetical protein.
DR				DR	SEQUENCE 227 AA; 25035 MW; 3FA0271A86E45FE CRC64;
KW				KW	Best Local Similarity 100.0%; Score 106; DB 2; Length 227; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY				QY	1 EVEDVPGVVEPASGHGEGGER 20
Db				Db	47 EVEDVPGVVEPASGHGEGGER 66
RESULT 2		PRELIMINARY:		PRT:	432 AA.
ID	051953	AC	051953	DT	01-JUN-1998 (TREMBLrel. 06, Created)
				DT	01-JUN-1998 (TREMBLrel. 06, Last sequence update)
				DT	01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DB				DB	Acidic repeat protein.
OS				OS	Treponema pallidum.
OC				OC	Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
RN				RN	NCBI_TaxID=160;
RP				RP	SEQUENCE FROM N.A.

GenCore version 5.1.6

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OM nucleic - nucleic search, using sw model

Run on: March 23, 2005, 10:23:13 ; Search time 7357.76 Seconds

10846.472 Million cell updates/sec

Title: US-10-017-168-19

Perfect score: 1647

Sequence: 1 atgttttgtgcgcgtgacat.....ttctgaaaaggcgccatga 1647

Scoring table: IDENTITY_NUC

GapOp 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Post-processing: Listing first 45 summaries

Database : GenBmbl:*

1: gb_ba:*

2: gb_htg:*

3: gb_in:*

4: gb_on:*

5: gb_ox:*

6: gb_dat:*

7: gb_ph:*

8: gb_dl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_by:*

13: gb_un:*

14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

20 231 14.0 152618 10 ACI27593

21 230 14.0 165592 10 ACI22020

22 230 14.0 194387 10 ACI105989

23 230 14.0 194736 10 ACI26271

24 228 13.9 120487 10 ACI103637

25 227 13.8 199378 2 ACI08255

26 225 13.6 171593 10 ACI12052

27 226 13.6 152435 10 ACI21566

28 225 13.7 237814 10 AC091464

29 225 13.7 187877 10 AL928735

30 223 13.6 240931 2 ACI07097

31 223 13.6 76341 10 BX000658

32 223 13.6 157754 10 ACI132313

33 221 13.5 187126 10 ACI13315

34 221 13.4 979339 2 ACI141520

35 221 13.4 215745 10 ACI17595

36 221 13.4 234888 2 ACI102097

37 220 13.4 195630 10 AC098726

38 220 13.4 157152 10 ACI146729

39 216 13.1 169003 10 ACI156599

40 216 13.1 178501 10 ACI121862

41 214 13.0 260225 2 AC096018

42 214 13.0 248718 10 ACI17629

43 213 13.0 217353 10 ACI149611

44 212 12.9 211547 10 ACI07828

45 212 12.9 171570 10 AL807807

ALIGNMENTS

20 231 14.0 152618 10 ACI127593

21 230 14.0 165592 10 ACI122020

22 230 14.0 194387 10 ACI105989

23 230 14.0 194736 10 ACI126271

24 228 13.9 120487 10 ACI103637

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45 212 12.9 171570 10 AL807807

ACI127593 Mus muscu

ACI122020 Mus muscu

ACI105989 Mus muscu

ACI126271 Mus muscu

ACI103637 Mus muscu

ACI12052 Rattus no

ACI132313 Mus muscu

ACI13315 Mus muscu

ACI141520 Rattus no

ACI17595 Mus muscu

ACI2097 Mus muscu

AC098726 Mus muscu

ACI146729 Mus muscu

ACI156599 Mus muscu

ACI121862 Mus muscu

AC096018 Rattus no

ACI17629 Mus muscu

ACI149611 Mus muscu

ACI07828 Mus muscu

AL807807 Mouse DNA

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ACI127593 Mus muscu

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ACI13315 Mus muscu

ACI141520 Rattus no

ACI17595 Mus muscu

ACI2097 Mus muscu

AC098726 Mus muscu

ACI146729 Mus muscu

ACI156599 Mus muscu

ACI121862 Mus muscu

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ACI17629 Mus muscu

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AL807807 Mouse DNA

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35 221 13.4 215745 10 ACI17595

36 221 13.4 234888 2 ACI102097

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40 216 13.1 178501 10 ACI121862

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42 214 13.0 248718 10 ACI17629

43 213 13.0 217353 10 ACI149611

44 212 12.9 211547 10 ACI07828

45 212 12.9 171570 10 AL807807

ACI127593 Mus muscu

ACI122020 Mus muscu

ACI105989 Mus muscu

ACI126271 Mus muscu

ACI103637 Mus muscu

ACI12052 Rattus no

ACI132313 Mus muscu

ACI13315 Mus muscu

ACI141520 Rattus no

ACI17595 Mus muscu

ACI2097 Mus muscu

AC098726 Mus muscu

ACI146729 Mus muscu

ACI156599 Mus muscu

ACI121862 Mus muscu

AC096018 Rattus no

ACI17629 Mus muscu

ACI149611 Mus muscu

ACI07828 Mus muscu

AL807807 Mouse DNA

20 231 14.0 152618 10 ACI127593

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23 230 14.0 194736 10 ACI126271

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28 225 13.7 237814 10 AC091464

29 225 13.7 187877 10 AL928735

30 223 13.6 240931 2 ACI07097

31 223 13.6 76341 10 BX000658

32 223 13.6 157754 10 ACI132313

33 221 13.5 187126 10 ACI13315

34 221 13.4 979339 2 ACI141520

35 221 13.4 215745 10 ACI17595

36 221 13.4 234888 2 ACI102097

37 220 13.4 195630 10 AC098726

38 220 13.4 157152 10 ACI146729

39 216 13.1 169003 10 ACI156599

40 216 13.1 178501 10 ACI121862

41 214 13.0 260225 2 AC096018

42 214 13.0 248718 10 ACI17629

43 213 13.0 217353 10 ACI149611

44 212 12.9 211547 10 ACI07828

45 212 12.9 171570 10 AL807807

ACI127593 Mus muscu

ACI122020 Mus muscu

ACI105989 Mus muscu

ACI126271 Mus muscu

ACI103637 Mus muscu

ACI12052 Rattus no

ACI132313 Mus muscu

ACI13315 Mus muscu

ACI141520 Rattus no

ACI17595 Mus muscu

ACI2097 Mus muscu

AC098726 Mus muscu

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ACI156599 Mus muscu

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ACI17629 Mus muscu

ACI149611 Mus muscu

ACI07828 Mus muscu

AL807807 Mouse DNA

20 231 14.0 152618 10 ACI127593

21 230 14.0 165592 10 ACI122020

22 230 14.0 194387 10 ACI105989

23 230 14.0 194736 10 ACI126271

24 228 13.9 120487 10 ACI103637

25 227 13.8 199378 2 ACI08255

26 225 13.6 171593 10 ACI12052

27 226 13.6 152435 10 ACI21566

28 225 13.7 237814 10 AC091464

29 225 13.7 187877 10 AL928735

30 223 13.6 240931 2 ACI07097

31 223 13.6 76341 10 BX000658

32 223 13.6 157754 10 ACI132313

33 221 13.5 187126 10 ACI13315

34 221 13.4 979339 2 ACI141520

35 221 13.4 215745 10 ACI17595

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29 225 13.7 187877 10 AL928735

30 223 13.6 240931 2 ACI07097

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36 221 13.4 234888 2 ACI102097

37 220 13.4 195630 10 AC098726

38 220 13.4 157152 10 ACI146729

39 216 13

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On nucleic - nucleic search, using SW model

Run on: March 23, 2005, 10:23:14 ; Search time 5849 Seconds
(without alignments)
10718.395 Million cell updates/sec

Title: US-10-017-168-19
perfect score: 1647
Sequence: 1 atgttttgccgactgtacat.....ttctgaaaaaggccgcgtatg 1647

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34230544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_htc:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gbs1:*

9: gb_gbs2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
C 1	204.8	12.4	1484 9	CL079800 CH216-156
C 2	203.2	12.3	905 9	CR071027 Forward 8
C 3	201.2	12.2	1204 8	CC284084 CH261-167
C 4	200.8	12.2	1047 6	CB905697 tric075x1
C 5	200.8	12.2	1047 7	CP877361 tric075x1
C 6	200.8	12.2	1178 9	CG751365 P045-4-D0
C 7	200.8	12.2	1314 9	CG748456 R042-2-D1
C 8	200.6	12.2	1170 8	CC291804 CH261-61G
C 9	200.6	12.2	1200 8	CC187380 CH261-133E
C 10	200	12.1	1297 9	CG744520 P037-1-B1
C 11	199.6	12.1	1309 9	CL080508 CH216-158
C 12	199.4	12.1	1292 8	CC208790 CH261-26P
C 13	199.2	12.1	911 9	CR116264 Forward 8
C 14	199	12.1	1874 9	AG448338 Mus muscu
C 15	198.8	12.1	1448 8	CC220110 CH261-92P
C 16	198.6	12.1	1066 6	CB905393 tric075x1
C 17	198.6	12.1	1056 7	CR87620 tric075x1
C 18	198.6	12.1	1068 9	AG429516 Mus muscu
C 19	198.6	12.1	1351 8	CC312666 TAN3-2-2D
C 20	198.6	12.1	1471 9	CG748176 R042-1-A0
C 21	198.2	12.0	845 9	CC578225 CH240 457
C 22	198.2	12.0	1223 9	AG441637 Mus muscu
C 23	198	12.0	1107 6	CB90529 tric075x1
C 24	198	12.0	1107 7	CF877385 tric075x1

ALIGNMENTS

RESULT 1
CL079800/c

DEFINITION CH216-156023_Sps1 CH216 Xenopus tropicalis genomic clone
CH216-156023, genomic survey sequence.

ACCESSION CL079800

VERSION 1

KEYWORDS GI:40535713

SOURCE GSS.

ORGANISM Xenopus tropicalis (western clawed frog)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus; Silurana.

REFERENCE 1 (bases 1 to 1484)

A physical map of the xenopus tropicalis genome
Unpublished (2003)

AUTHORS Kremitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T., Mardis, B. and Wilson, R.

TITLE A physical map of the xenopus tropicalis genome

JOURNAL Unpublished (2003)

COMMENT Contact: Richard K Wilson

Genome Sequencing Center
Washington University School of Medicine
Email: submissions@wuston.wustl.edu
Insert Length: 175000 Std Err: 0.00
Seq primer: Sps atctggcggttcgcaccc
Class: BAC ends

FEATURES High quality sequence start: 549
High quality sequence stop: 627.

SOURCE 1. Location/Qualifiers
/organism="Xenopus tropicalis"
/mol_type="genomic DNA"
/strain="Nigerian frog"
/db_xref="Taxon:8364"
/clone="CH216-156023"
/sex="male"
/cell_line="Stock 248 F7A2, inbred N7"
/clone_lib="CH216"
/note="vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis BAC library"

ORIGIN

Query Match Score 204.8; DB 9; Length 1484;
Best Local Similarity 51.5%; Pred. No. 1.2e-42; Mismatches 437; Conservative 0; Indels 0; Gaps 0;

QY 380 GTGAGGTTGAGGACCGCCAGGTAGTAGGAGCCCTGAGCGTGAAGGAGGGAGC 439

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On nucleic - nucleic search, using sw model

Run on: March 23, 2005, 10:23:13 ; Search time 929.12 Seconds

(without alignments) 10493.597 Million cell updates/sec

Title: US-10-017-168-19

Perfect score: 1647

Sequence: 1 atgttgtgtgcgcgtgacat.....ttctgaaaaggcgcatga 1647

Scoring table: IDENTITY NUC

Gappen 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959970667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_168ec04,*
1: geneseqn1980s:*

2: geneseqn1990s:*

3: geneseqn2000s:*

4: geneseqn2001s:*

5: geneseqn2001b:*

6: geneseqn2002a:*

7: geneseqn2002b:*

8: geneseqn2003a:*

9: geneseqn2003s:*

10: geneseqn2003c:*

11: geneseqn2003ds:*

12: geneseqn2004as:*

13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
1	1534.4	99.2	2945	4 AAC94547	Aac94547 T. pallid
2	858.4	52.1	939	4 AAC84649	Aac84649 T. pallid
3	695.8	42.2	9410	2 AAC20603	Aac20603 Polynucleic Acid
4	621.6	37.7	699	4 AAC84648	Aac84648 T. pallid
5	206.4	12.5	1926	10 ADK65580	Adk65580 Human hair
6	206.2	12.5	1926	3 AAC50254	Aac50254 Epstein-Barr virus
7	206.2	12.5	1926	4 AAF82902	Aaf82902 EBV tRNA
8	206.2	12.5	2580	3 AAC75454	Aac75454 Nucleic acid
9	206.2	12.5	2580	6 AAI16427	Aai164275 Epstein-Barr virus
10	206.2	12.5	5452	2 AAE23778	Aax91923 Anti-sense
11	206.2	12.5	8705	2 AAE23778	Aaz23778 Vector PS
12	206.2	12.5	8705	12 ADM10559	Adm10559 Expresso
13	206.2	12.5	9482	12 ADP64415	Adp64415 Vector PC
14	206.2	12.5	9800	2 AAV21683	Aav21683 Vector pl
15	206.2	12.5	10285	6 ABS11027	Ab871027 PCEP-1a-F
16	206.2	12.5	10285	6 ABS66453	Ab866453 Plasmid p
17	206.2	12.5	10330	12 ADL67154	Adl67154 Plasmid p
18	206.2	12.5	10380	2 AAZ22248	Aaz22248 Nucleic acid
19	206.2	12.5	10477	12 ADL67152	Adl67152 Plasmid p
20	206.2	12.5	10516	12 ADL67150	Adl67150 Plasmid p

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_168ec04,*

1: geneseqn1980s:*

2: geneseqn1990s:*

3: geneseqn2000s:*

4: geneseqn2001s:*

5: geneseqn2001b:*

6: geneseqn2002a:*

7: geneseqn2002b:*

8: geneseqn2003a:*

9: geneseqn2003s:*

10: geneseqn2003c:*

11: geneseqn2003ds:*

12: geneseqn2004as:*

13: geneseqn2004bs:*

ALIGMENTS

RESULT 1

AAC84647

ID AAC84647 standard; DNA; 2945 BP.

XX AAC84647;

XX DT 11-SEP-2003 (revised)

XX DT 20-APR-2001 (first entry)

XX DE T. pallidum acidic repeat protein (arp) encoding DNA.

XX KW Treponema pallidum; acidic repeat protein; arp; immunogenic; syphilis; yawb; bejel; ds.

XX OS Treponema pallidum; ssp. pallidum.

XX FH location/Qualifiers

XX FT 919 .2217

XX FT CDS

XX FT /*tag= a

ALIGMENTS

C	21	206.2	12.5	10561	12 ADL67148	Adl67148 Plasmid p
C	22	206.2	12.5	10596	2 AAO51731	Aao51731 Plasmid p
C	23	206.2	12.5	10596	2 AAX15650	Aax15650 Nucleotid
C	24	206.2	12.5	10596	2 AAT0348	Aat0348 Plasmid p
C	25	206.2	12.5	10615	12 ADL67175	Adl67175 Plasmid p
C	26	206.2	12.5	10774	12 ADL67153	Adl67153 Plasmid p
C	27	206.2	12.5	10921	12 ADL67151	Adl67151 Plasmid p
C	28	206.2	12.5	10961	12 ADL67149	Adl67149 Plasmid p
C	29	206.2	12.5	11006	12 ADL67147	Adl67147 Plasmid p
C	30	206.2	12.5	11059	12 ADL67176	Adl67176 Plasmid p
C	31	206.2	12.5	11693	13 ADL12379	Adl12379 Vector PC
C	32	206.2	12.5	11924	12 ADL07395	Adl07395 Modified
C	33	206.2	12.5	12242	12 ADL07394	Adl07394 Modified
C	34	206.2	12.5	16080	3 AAM59530	Aam59530 DNA clone
C	35	206.2	12.5	17753	12 ADL17110	Adl17110 Expressio
C	36	206.2	12.5	17781	12 ADL12161	Adl12161 Spotein-B
C	37	203.6	12.4	12733	6 ARK8631	Ark8631 Vector PE
C	38	203.6	12.4	12733	9 ACD13882	Adc13882 L. lactis
C	39	203.6	12.4	12739	9 ACD13843	Adc13843 Vector PE
C	40	203.6	12.4	12739	9 ACD13843	Adc13843 Plasmid p
C	41	199.8	12.3	30191	12 ADD9754	Adg9754 Mouse can
C	42	199.8	12.1	19251	12 AAX09224	Aax0924 Epstein B
C	43	191.2	11.6	799	2 AAV5831	Aav5831 Nucleotid
C	44	177.8	10.8	795	2 AAV5830	Aav5830 F16A inse
C	45	163.8	9.9	3127	12 ADN12154	Adn12154 Kaposis B

The invention relates to a method of detecting presence of Treponema